

1201 GTTGTGTTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
1201 GTTGTGTTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
1261 GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGTTC 1320
1261 GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGTTC 1320
1321 ATAGGTGAGGGCTGGGCTTTGTTCAAAAGTTATCATCTAAATTAACAGACTCGAGCC 1380
1321 ATAGGTGAGGGCTGGGCTTTGTTCAAAAGTTATCATCTAAATTAACAGACTCGAGCC 1380
1381 CACTCCCTGTGACCCCTGGGTGATCGGGAGCAGGSCCAGAAATCAAACCTTAACTTTCT 1440
1381 CACTCCCTGTGACCCCTGGGTGATCGGGAGCAGGSCCAGAAATCAAACCTTAACTTTCT 1440
1441 TATTCGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCTCTCGGGGGAGAA 1500
1441 TATTCGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCTCTCGGGGGAGAA 1500
1501 GTCAATTAATTAATGAAATCTCATCATGTCCACCCGAGGAGGGCTTCTGACTGTGGTTCG 1560
1501 GTCAATTAATTAATGAAATCTCATCATGTCCACCCGAGGAGGGCTTCTGACTGTGGTTCG 1560
1561 CTTGACAGTATATCCGAAAGGTGCGGAGAGGGGGTGTGAAAGATGCCATTTTCTTCT 1620
1561 CTTGACAGTATATCCGAAAGGTGCGGAGAGGGGGTGTGAAAGATGCCATTTTCTTCT 1620
1621 CCAGCGGTAACTGGTGGCGGGTGGACGAGCCAGCGGGCGGGGAGGATCTGGCCAG 1680
1621 CCAGCGGTAACTGGTGGCGGGTGGACGAGCCAGCGGGCGGGGAGGATCTGGCCAG 1680
1681 ATGGCTGCGGGGGGGTGTCTTCTTCTCGGTAAAGCCCTCTTGGATAGTCAATCTGA 1740
1681 ATGGCTGCGGGGGGGTGTCTTCTTCTCGGTAAAGCCCTCTTGGATAGTCAATCTGA 1740
1741 AAACGAAAGAGTGCCTCTGAAGTATT 1767
1741 AAACGAAAGAGTGCCTCTGAAGTATT 1767

RESULT 2
US-10-682-420-19/c
; Sequence 19, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 19
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Type B Pwd circovirus

US-10-682-420-19
Query Match 100.0%; Score 1767; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGAGCAGCTTGGCAGCGGAGCAGCTCCGAGCAGCCTCAGCAGCAACATGCCCGCA 60
DB 1767 ACCGAGCAGCTTGGCAGCGGAGCAGCTCCGAGCAGCCTCAGCAGCAACATGCCCGCA 1708
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAAGGTGGGTGTTCACTCTGAATAATC 120
DB 1707 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAAGGTGGGTGTTCACTCTGAATAATC 1648
QY 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATATTTTA 180
DB 1647 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATATTTTA 1588
QY 181 TTGTTGGCAGAGAGGTTAATGAGGAAGACGAAACACCTCACCTCCAGGGGTTTCGCTAAT 240
DB 1587 TTGTTGGCAGAGAGGTTAATGAGGAAGACGAAACACCTCACCTCCAGGGGTTTCGCTAAT 1528
QY 241 TTGTCGAAGACGAGACTTTTAAATAAGTGAAGTGTATTTGGGTGCCCGCTCCACATCG 300
DB 1527 TTGTCGAAGACGAGACTTTTAAATAAGTGAAGTGTATTTGGGTGCCCGCTCCACATCG 1468
QY 301 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATCTGCAGTAAAGAAAGCAACTTAC 360
DB 1467 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATCTGCAGTAAAGAAAGCAACTTAC 1408
QY 361 TGATCGAGTGTGAGCTCCTAGATCTCAGGGACAAAGGAGTGACCTGTCTACTGTGTGA 420
DB 1407 TGATCGAGTGTGAGCTCCTAGATCTCAGGGACAAAGGAGTGACCTGTCTACTGTGTGA 1348
QY 421 GTACCTTGTGAGAGCGGGAGTCTGTGACCGTTGACAGCAGCAACCTGTAAACGTTTG 480
DB 1347 GTACCTTGTGAGAGCGGGAGTCTGTGACCGTTGACAGCAGCAACCTGTAAACGTTTG 1288
QY 481 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATGCAAGACGCTG 540
DB 1287 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATGCAAGACGCTG 1228
QY 541 ATTTGAAAGACTAATGTACAGTCAATTTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600
DB 1227 ATTTGAAAGACTAATGTACAGTCAATTTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 1168
QY 601 CTGCTAATTTTCAGACCCGGAACACATCTGGAACCCACCTAGAAAACAGTGTGGG 660
DB 1167 CTGCTAATTTTCAGACCCGGAACACATCTGGAACCCACCTAGAAAACAGTGTGGG 1108
QY 661 ATGGTTACCATGTTGAAGAGTGGTTTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 1107 ATGGTTACCATGTTGAAGAGTGGTTTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1048
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGACTGTAGAGACTAAGGTGGAACTG 780
DB 1047 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGACTGTAGAGACTAAGGTGGAACTG 988
QY 781 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAAATGCTACT 840
DB 987 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAAATGCTACT 928
QY 841 CTTCAACTGCTGTCGCCAGCTGTAGAGCTCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 927 CTTCAACTGCTGTCGCCAGCTGTAGAGCTCTTTTATCGGAGGATTAATCTCTTGGTATTTT 868
QY 901 GGAAGAAATGCTACAGAAACAATCCAGAGGAAAGGGGGCAGTTCGTACCCCTTCCCGCC 960
DB 867 GGAAGAAATGCTACAGAAACAATCCAGAGGAAAGGGGGCAGTTCGTACCCCTTCCCGCC 808
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATGACTCTTTTTTATCACTTCCTCAATGGT 1020
DB 807 CATGCCCTGAATTTCCATATGAATAAATTAATGACTCTTTTTTATCACTTCCTCAATGGT 748

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Qy 1021 TTTTATTATTCAATTAAGGTTAAGTGGGGGCTTTTAAATTAATTTCTCTGAATTCGTAC 1080
Db 747 TTTTATTATTCAATTAAGGTTAAGTGGGGGCTTTTAAATTAATTTCTCTGAATTCGTAC 688
Qy 1081 ATACATGGTTACACGGATATTGTATTCCTGTCGTATATATCTGTTTCGAACGAGTGCC 1140
Db 687 ATACATGGTTACACGGATATTGTATTCCTGTCGTATATATCTGTTTCGAACGAGTGCC 628
Qy 1141 GAGCCTACGTGGTCTACATTTCCAGCAAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
Db 627 GAGCCTACGTGGTCTACATTTCCAGCAAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 568
Qy 1201 GTTGTGGTTGGAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTACCG 1260
Db 567 GTTGTGGTTGGAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTACCG 508
Qy 1261 GGAGTGGTAGGAGGAGGCTGGGTTTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 1320
Db 507 GGAGTGGTAGGAGGAGGCTGGGTTTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 448
Qy 1321 ATAGGTAGGCTGTGGCTTTGTTTCAAAAGTTATCATCTAAATTAACAGCACTGGAGCC 1380
Db 447 ATAGGTAGGCTGTGGCTTTGTTTCAAAAGTTATCATCTAAATTAACAGCACTGGAGCC 388
Qy 1381 CACTCCCTGTCACTCCCTGGGTGATCGGGGAGCGGCGGAGGAGTCAACCTTTAACTTTCT 1440
Db 387 CACTCCCTGTCACTCCCTGGGTGATCGGGGAGCGGCGGAGGAGTCAACCTTTAACTTTCT 328
Qy 1441 TATTCTGTAGTATTCAAAAGGACACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 1500
Db 327 TATTCTGTAGTATTCAAAAGGACACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 268
Qy 1501 GTCAATTAATTAATCAATCATCATGTCCACCGCCACAGAGGCGGTTCTGACTGGTTTCG 1560
Db 267 GTCAATTAATTAATCAATCATCATGTCCACCGCCACAGAGGCGGTTCTGACTGGTTTCG 208
Qy 1561 CTTGACAGTATATCGAAGGTCGGGAGCGGGGTGTTGAAGTGCATTTTCTCTTCT 1620
Db 207 CTTGACAGTATATCGAAGGTCGGGAGCGGGGTGTTGAAGTGCATTTTCTCTTCT 148
Qy 1621 CCAGCGGTAAACGTCGGCGGGTGGAGCGAGCGGGGCGGCGGAGGATCTGGCCAAAG 1680
Db 147 CCAGCGGTAAACGTCGGCGGGTGGAGCGAGCGGGGCGGCGGAGGATCTGGCCAAAG 88
Qy 1681 ATGGCTGGCGGGGCGGTGTCTTCTTCGTGTAACGCTCTCTGATAGCTCATATCTGA 1740
Db 87 ATGGCTGGCGGGGCGGTGTCTTCTTCTGTAACGCTCTCTGATAGCTCATATCTGA 28
Qy 1741 AAACGAAAGAACTGCGCTCTAAGTATT 1767
Db 27 AAACGAAAGAACTGCGCTCTAAGTATT 1

RESULT 3
US-10-409-613-15
; Sequence 15, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
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i LOCATION: (1741)..(1767)
US-10-409-613-15

Query Match 100.0%; Score 1767; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60
Db 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60

Qy 61 AGAAGAATGGAAGAGCGGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 120
Db 61 AGAAGAATGGAAGAGCGGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 120

Qy 121 CTTCCGAGAGCGGCGAGCAAGAAATACGGGATCTTCCAAATCCCTATTTCGATTAATTTA 180
Db 121 CTTCCGAGAGCGGCGAGCAAGAAATACGGGATCTTCCAAATCCCTATTTCGATTAATTTA 180

Qy 181 TTGTTGGCGAGGAGGTAAATGAGGAAGCAACACCTCACCTCCAGGGGTTTCGCTAATT 240
Db 181 TTGTTGGCGAGGAGGTAAATGAGGAAGCAACACCTCACCTCCAGGGGTTTCGCTAATT 240

Qy 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
Db 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300

Qy 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATACGCAAGTAAGAGCAACTTAC 360
Db 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATACGCAAGTAAGAGCAACTTAC 360

Qy 361 TCAATGAGTGTGAGCTCTAGACTCAGGGAACAGGAGTCACTGTCTACTGTGTA 420
Db 361 TCAATGAGTGTGAGCTCTAGACTCAGGGAACAGGAGTCACTGTCTACTGTGTA 420

Qy 421 GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTTCAGAGCAGCAACCTGTAAAGTTG 480
Db 421 GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTTCAGAGCAGCAACCTGTAAAGTTG 480

Qy 481 TCAGAAATTTCCGGCGGTGGCTGAACCTTTGAAAGTGAAGCGGAAATGCAAGACGCTG 540
Db 481 TCAGAAATTTCCGGCGGTGGCTGAACCTTTGAAAGTGAAGCGGAAATGCAAGACGCTG 540

Qy 541 ATTGGAAGCTAATGTACAGCTCATTGTGGGCGCACTCGGTGTGTAAAGCAATGG 600
Db 541 ATTGGAAGCTAATGTACAGCTCATTGTGGGCGCACTCGGTGTGTAAAGCAATGG 600

Qy 601 CTGCTAATTTTGCAGACCCCGGAAACCAATACCTAGGAAACCACTAGAAACAAAGTGGTGG 660
Db 601 CTGCTAATTTTGCAGACCCCGGAAACCAATACCTAGGAAACCACTAGAAACAAAGTGGTGG 660

Qy 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 720
Db 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 720

Qy 721 ATGATCTACTGAGCTGTGATCGATATCCATTTGATGACTTTTATGGCTGGCTGGCTGG 780
Db 721 ATGATCTACTGAGCTGTGATCGATATCCATTTGATGACTTTTATGGCTGGCTGGCTGG 780

Qy 781 TACCTTTTGGCCCCCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
Db 781 TACCTTTTGGCCCCCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840

Qy 841 CCTCAACTGCTGCCAGCTGTAGAAGCTTTTATCGAGGATTAATCTCTGGTATTTT 900
Db 841 CCTCAACTGCTGCCAGCTGTAGAAGCTTTTATCGAGGATTAATCTCTGGTATTTT 900

Qy 901 GGAAGATGCTACAGCAACATCCACGAGAGGGGGCCAGTTCCGTCACCTTTCCCGCC 960
Db 901 GGAAGATGCTACAGCAACATCCACGAGAGGGGGCCAGTTCCGTCACCTTTCCCGCC 960

Qy 961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Db 961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020

RESULT 4
US-10-409-613-19/c
; Sequence 19, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CAROLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; FILE REFERENCE: 065691/0176

Db 961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAAT 1020
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Db 1021 TTTTATTATTTCATTAAGGGTTAAGTGGGGGTCTTTAAAAATTAATTTCTCTGAATGTAC 1080
Qy 1081 ATACATGTTACAGGATATTTGTTTCTGCTGATATATCTGTTTTCGACGAGTGGC 1140
Db 1081 ATACATGTTACAGGATATTTGTTTCTGCTGATATATCTGTTTTCGACGAGTGGC 1140
Qy 1141 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
Db 1141 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
Qy 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACG 1260
Db 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACG 1260
Qy 1261 GGAGTGTAGGAGAGGGCTGGTTATGTTATGCGGAGGAGTAGTATTACATAGGGTC 1320
Db 1261 GGAGTGTAGGAGAGGGCTGGTTATGTTATGCGGAGGAGTAGTATTACATAGGGTC 1320
Qy 1321 ATAGTGAAGGCTGTGGCTTTTACAAAGTTATCATCTAAATAACAGCACTTGAGCC 1380
Db 1321 ATAGTGAAGGCTGTGGCTTTTACAAAGTTATCATCTAAATAACAGCACTTGAGCC 1380
Qy 1381 CACTCCCTGTCACTGGGTGATCGGGAGCAGGCGCCAGAAATCAACCTTTAACCTTTCT 1440
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Qy 1561 CTTGACAGTATATCCGAAGGTGCGGAGGAGGCGGTGTTGAAGATGCCATTTTCTTCT 1620
Db 1561 CTTGACAGTATATCCGAAGGTGCGGAGGAGGCGGTGTTGAAGATGCCATTTTCTTCT 1620
Qy 1621 CCAGCGGTAAACGTTGCGGGGGTGAACAGCCAGCGGGGCGCGGAGGAGTCTGGCCAAG 1680
Db 1621 CCAGCGGTAAACGTTGCGGGGGTGAACAGCCAGCGGGGCGCGGAGGAGTCTGGCCAAG 1680
Qy 1681 ATGGCTGCGGGGCGGTGTTCTTCTTCTGTAACGCTTCTTGGATAGTCTATCTGA 1740
Db 1681 ATGGCTGCGGGGCGGTGTTCTTCTTCTGTAACGCTTCTTGGATAGTCTATCTGA 1740
Qy 1741 AAAACGAAGAAGTGGCTGTAAAGTATT 1767
Db 1741 AAAACGAAGAAGTGGCTGTAAAGTATT 1767

CURRENT APPLICATION NUMBER: US/10/409,613	
CURRENT FILING DATE: 2003-04-09	
PRIOR APPLICATION NUMBER: US/09/514,245B	
PRIOR FILING DATE: 2000-02-28	
PRIOR APPLICATION NUMBER: FR 97/15396	
PRIOR FILING DATE: 1997-12-05	
NUMBER OF SEQ ID NOS: 170	
SOFTWARE: PatentIn version 3.0	
SEQ ID NO 19	
LENGTH: 1767	
TYPE: DNA	
ORGANISM: Type B PWD circovirus	
US-10-409-613-19	
Query Match 100.0%; Score 1767; DB 16; Length 1767;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1	ACCAGCGCACTTCGGCAGCGGAGCACCCTCGCAGCACCTCAGCAGCAATGCCAGCA 60
Db	
Qy 61	AGAGAAATGGAGAGCGGACCCCAACCCATAAAGGTGGGTGTTCACTCTGAATAATC 120
Db	
Qy 1707	AGAGAAATGGAGAGCGGACCCCAACCCATAAAGGTGGGTGTTCACTCTGAATAATC 1648
Db	
Qy 121	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCCAATATCCCTATTTGATTTTA 180
Db	
Qy 1647	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCCAATATCCCTATTTGATTTTA 1588
Db	
Qy 181	TTGTTGGCAGAGAGGGTAATGAGGAGGACGAAACACCTCACCCTCAGGGGTTCCGTAAT 240
Db	
Qy 1587	TTGTTGGCAGAGAGGGTAATGAGGAGGACGAAACACCTCACCCTCAGGGGTTCCGTAAT 1528
Db	
Qy 241	TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
Db	
Qy 1527	TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 1468
Db	
Qy 301	AGAAAGCGAAAGAAACAGATACGAGAAATAAGAGATCTGCGAGTAAAGAGCAACTTAC 360
Db	
Qy 1467	AGAAAGCGAAAGAAACAGATACGAGAAATAAGAGATCTGCGAGTAAAGAGCAACTTAC 1408
Db	
Qy 361	TGATGAGTGTGGAGCTCTAGATCTCAGGACCAAGAGTACCTGCTACTGCTGTA 420
Db	
Qy 1407	TGATGAGTGTGGAGCTCTAGATCTCAGGACCAAGAGTACCTGCTACTGCTGTA 1348
Db	
Qy 421	GTACCTTTGTTGAGAGCGGAGTCTGGTGAACCGTTGCGAGAGCAACCTGTAAAGTTG 480
Db	
Qy 1347	GTACCTTTGTTGAGAGCGGAGTCTGGTGAACCGTTGCGAGAGCAACCTGTAAAGTTG 1288
Db	
Qy 481	TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATGCAAGACGTG 540
Db	
Qy 1287	TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATGCAAGACGTG 1228
Db	
Qy 541	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACTGGGTGTGTTAAAGCAATGG 600
Db	
Qy 1227	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACTGGGTGTGTTAAAGCAATGG 1168
Db	
Qy 601	CTGCTAATTTTGCAGACCCGGAAACCACTATCTGGAAACCACTATGGAACCAAGTGGTGG 660
Db	
Qy 1167	CTGCTAATTTTGCAGACCCGGAAACCACTATCTGGAAACCACTATGGAACCAAGTGGTGG 1108
Db	
Qy 661	ATGGTTACCAATGGTGAAGAGTGGTGTATTTGATGACTTTATGGCTGCTCCCTGGG 720
Db	
Qy 1107	ATGGTTACCAATGGTGAAGAGTGGTGTATTTGATGACTTTATGGCTGCTCCCTGGG 1048
Db	
Qy 721	ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGACATAAAGTTGGAATCG 780
Db	
Qy 1047	ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGACATAAAGTTGGAATCG 988
Db	
Qy 781	TACCTTTTGGCCCGCAGTATTTCTGATTTACCAGCAATCAGCCCGTTCGAAATGGTACT 840
Db	
Qy 987	TACCTTTTGGCCCGCAGTATTTCTGATTTACCAGCAATCAGCCCGTTCGAAATGGTACT 928
Db	

RESULT 5
US-10-442-180-15
; Sequence 15, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel

1741 AAACGAAAGAGTGGCTGTAAATTT 1767
27 AAACGAAAGAGTGGCTGTAAATTT 1

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APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Philippe
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PMD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: US/09/514,245
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 1767
TYPE: DNA
ORGANISM: Type B PWD circovirus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(111)
FEATURE:
NAME/KEY: CDS
LOCATION: (115)..(243)
FEATURE:
NAME/KEY: CDS
LOCATION: (247)..(267)
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NAME/KEY: CDS
LOCATION: (271)..(360)
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NAME/KEY: CDS
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LOCATION: (514)..(516)
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LOCATION: (1177)..(1233)
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LOCATION: (1237)..(1359)
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LOCATION: (1363)..(1476)
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NAME/KEY: CDS
LOCATION: (1480)..(1737)
FEATURE:
NAME/KEY: CDS
LOCATION: (1741)..(1767)
US-10-442-180-15
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Query Match 100.0%; Score 1767; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGGCAGCGGACACCTCGCGAGCACCTCAGCAGCAACATGCCCAGCA 60
DB 1 ACCAGCGCACTTCGGCAGCGGACACCTCGCGAGCACCTCAGCAGCAACATGCCCAGCA 60

QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGAATAATC 120
DB 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGAATAATC 120

QY 121 CTTCCGAAGACGAGCGGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATTTT 180
DB 121 CTTCCGAAGACGAGCGGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATTTT 180

QY 181 TTGTTGGCAGGAGGGTAAATGAGGAAGACGAAACACCTCACCTCCAGGGGTTCCGTAATT 240
DB 181 TTGTTGGCAGGAGGGTAAATGAGGAAGACGAAACACCTCACCTCCAGGGGTTCCGTAATT 240

QY 241 TTGTAAGAACGACACTTTTAAATAAAGTGAAGTGGTATTTGGTGCCCGCTGCCACATCG 300
DB 241 TTGTAAGAACGACACTTTTAAATAAAGTGAAGTGGTATTTGGTGCCCGCTGCCACATCG 300

QY 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATCTGCAGTAAAGGCAACTTAC 360
DB 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATCTGCAGTAAAGGCAACTTAC 360

QY 361 TGATGGAGTGTGGAGCTCTTAGATCTCAGGGACAAACGAGTGACCTGTCTACTGTGTA 420
DB 361 TGATGGAGTGTGGAGCTCTTAGATCTCAGGGACAAACGAGTGACCTGTCTACTGTGTA 420

QY 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTTGCAGAGCAGCACCTGTAACTTTG 480
DB 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTTGCAGAGCAGCACCTGTAACTTTG 480

QY 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAAGGGAATAATGCAGAACGCTG 540
DB 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAAGGGAATAATGCAGAACGCTG 540

QY 541 ATTGGAAGACTAATGTACACGTCTTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600
DB 541 ATTGGAAGACTAATGTACACGTCTTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600

QY 601 CTGCTAATTTTGCAGACCCGGGAAACCAATCTTGGAAACCACTAGAAAACAGTGGTGGG 660
DB 601 CTGCTAATTTTGCAGACCCGGGAAACCAATCTTGGAAACCACTAGAAAACAGTGGTGGG 660

QY 661 ATGGTTACCATGTTGAAGAGTGGTGTATTTATGATGACTTTTATGGCTGGCTCCCTGGG 720
DB 661 ATGGTTACCATGTTGAAGAGTGGTGTATTTATGATGACTTTTATGGCTGGCTCCCTGGG 720

QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGACTCTAGAGACTAAAGGTGGA 780
DB 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGACTCTAGAGACTAAAGGTGGA 780

QY 781 TACCTTTTGGCCCGCAGTATTTGATTAACGAGCAATCAGACCCCGTTGGAATGGTACT 840
DB 781 TACCTTTTGGCCCGCAGTATTTGATTAACGAGCAATCAGACCCCGTTGGAATGGTACT 840
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Db	781	TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCGCTTGGAAAGGTACT	840
Qy	841	CCTCAACTGCTGTCACAGCTGTAGAAGCTCTTTATTCGGAGGATTACTCTCTTGGTATTTT	900
Db	841	CCTCAACTGCTGTCACAGCTGTAGAAGCTCTTTATTCGGAGGATTACTCTCTTGGTATTTT	900
Qy	901	GGAAAGTGTCTACAGAACAAATCCACGAGAGGAAGGGGCCAGTTCGTCACCTTTCCGCC	960
Db	901	GGAAAGTGTCTACAGAACAAATCCACGAGAGGAAGGGGCCAGTTCGTCACCTTTCCGCC	960
Qy	961	CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTATCATTCTGTAATGGT	1020
Db	961	CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTATCATTCTGTAATGGT	1020
Qy	1021	TTTTATTATTCAATTAGGGTTAAGTGGGGGCTCTTTAAATAATAATCTCTGAAATTGTAC	1080
Db	1021	TTTTATTATTCAATTAGGGTTAAGTGGGGGCTCTTTAAATAATAATCTCTGAAATTGTAC	1080
Qy	1081	ATACATGGTTACACGGATATTGTATTCTCTGGTCTGTATATACCTGTTTTCGAAAGCGTGC	1140
Db	1081	ATACATGGTTACACGGATATTGTATTCTCTGGTCTGTATATACCTGTTTTCGAAAGCGTGC	1140
Qy	1141	GAGGCTTACGTGGTCTACATTTCCAGCAGTTTCTGAGTCTCAGCCACAGCTGGTTTCTTTT	1200
Db	1141	GAGGCTTACGTGGTCTACATTTCCAGCAGTTTCTGAGTCTCAGCCACAGCTGGTTTCTTTT	1200
Qy	1201	GTTCCTTTGGTTGGAAGTAATAACAATGATGAAATCTTAGGACAGGTTTGGGGTAAAGTACC	1260
Db	1201	GTTCCTTTGGTTGGAAGTAATAACAATGATGAAATCTTAGGACAGGTTTGGGGTAAAGTACC	1260
Qy	1261	GGAGTGTGAGGAGAGGCTGGGTTATGTATGGCGGGAGGAGTAGTTTTACATAGGGTCT	1320
Db	1261	GGAGTGTGAGGAGAGGCTGGGTTATGTATGGCGGGAGGAGTAGTTTTACATAGGGTCT	1320
Qy	1321	ATAGGTGAGGCTGTGGCTTTGTTTACAAGTTATCATCTAAAATAACAGCACTGGAGCC	1380
Db	1321	ATAGGTGAGGCTGTGGCTTTGTTTACAAGTTATCATCTAAAATAACAGCACTGGAGCC	1380
Qy	1381	CACCTCCCCTGTCAACCTGGGTGATCGGGAGACAGGCCAGAAATCAACCTTAACCTTTCT	1440
Db	1381	CACCTCCCCTGTCAACCTGGGTGATCGGGAGACAGGCCAGAAATCAACCTTAACCTTTCT	1440
Qy	1441	TATTCGTGAGTATTCAAAGGACACAGCCGGGGGTTTGACCCCCCTCTCGGGGGAAGAA	1500
Db	1441	TATTCGTGAGTATTCAAAGGACACAGCCGGGGGTTTGACCCCCCTCTCGGGGGAAGAA	1500
Qy	1501	GTCATTAAATATTGAATCTCATCTGTCACCGCCGACAGAGGGCGCTTCTGACTGTGGTTCG	1560
Db	1501	GTCATTAAATATTGAATCTCATCTGTCACCGCCGACAGAGGGCGCTTCTGACTGTGGTTCG	1560
Qy	1561	CTTGCAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCGATTTTTTCTTCTTCT	1620
Db	1561	CTTGCAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCGATTTTTTCTTCTTCT	1620
Qy	1621	CCAGCGGTAAACGGTGGCGGGGTGACAGCACGGGGCGGCGGAGGATCTGGCCCAAG	1680
Db	1621	CCAGCGGTAAACGGTGGCGGGGTGACAGCACGGGGCGGCGGAGGATCTGGCCCAAG	1680
Qy	1681	ATGGCTGCGGGGGCGGTGTCTTCTTCTTCCGTAACGGCTCTCTGGATACGTCATATCTGA	1740
Db	1681	ATGGCTGCGGGGGCGGTGTCTTCTTCTTCCGTAACGGCTCTCTGGATACGTCATATCTGA	1740
Qy	1741	AAACGAAAGAGTGGCGCTGTAAGTATT	1767
Db	1741	AAACGAAAGAGTGGCGCTGTAAGTATT	1767

RESULT 6
US-10-442-180-19/c
; Sequence 19, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre

```

; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyn
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADSEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PMD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Type B PMD circovirus
US-10-442-180-19

Query Match 100.0%; Score 1767; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY	541	ATTGGAAGACTAATGTATACAGCTCATTTGTGGGGCCACTCGGTGTGGTAAAGCAAAATGGG	600
DB	541		
QY	541	ATTGGAAGAACCAATGTATACACTTCATTTGTGGGGCCACTCGGTGTGGTAAAGCAAAATGGG	600
DB	541		
QY	601	CTGCTAATTTTGCAGACCCGGAAACACATATCTGGAACCACTTAGAAACAAGTGGTGGG	660
DB	601		
QY	601	CTGCTAATTTTGCAGACCCGGAAACACATATCTGGAACCACTTAGAAACAAGTGGTGGG	660
DB	601		
QY	661	ATGGTTACCATGTGTGAAGAAGTGGTTGTTATTTGATGACCTTTATCGCTGGCTGCCCTGGG	720
DB	661		
QY	661	ATGGTTACCATGTGTGAAGAAGTGGTTGTTATTTGATGACCTTTATCGCTGGCTGCCCTGGG	720
DB	661		
QY	721	ATGATCTACTGAGACGTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACCTG	780
DB	721		
QY	721	ATGATCTACTGAGACGTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACCTG	780
DB	721		
QY	781	TACCTTTTTTGGCCCCGAGTATTCTGANTTACAGCAATCAGACCCCGTTTGGAAATGGTACT	840
DB	781		
QY	781	TACCTTTTTTGGCCCCGAGTATTCTGANTTACAGCAATCAGACCCCGTTTGGAAATGGTACT	840
DB	781		
QY	841	CCTCAACTGCTGCCAGCTGTAGAACTCTTTATCGGAGGATTACTCTCTTGGTATTTTT	900
DB	841		
QY	841	CCTCAACTGCTGCCAGCTGTAGAACTCTTTATCGGAGGATTACTCTCTTGGTATTTTT	900
DB	841		
QY	901	GGAAGAAATGCTACAGAAACAATCCACGAGGAAAGGGGCCAGTTTCGTCACCCCTTCCCCC	960
DB	901		
QY	901	GGAAGAAATGCTACAGAAACAATCCACGAGGAAAGGGGCCAGTTTCGTCACCCCTTCCCCC	960
DB	901		
QY	961	CATGCCCTGAAATTTCCATATGAAATAAATTAATCTGAGTCTTTTTTTATCATCTTGTAATGT	1020
DB	961		
QY	961	CATGCCCTGAAATTTCCATATGAAATAAATTAATCTGAGTCTTTTTTTATCATCTTGTAATGT	1020
DB	961		
QY	1021	TTTTATTATTCATTAAGGGTT-AGTGGGGGTCTTTAAATTAATAATCTCTGAAATGTA	1079
DB	1021		
QY	1021	TTTTATTATTCATTAAGGGTTCAAGTGGGGGTCTTTAAAGATTAATAATCTCTGAAATGTA	1080
DB	1021		
QY	1080	CATACATGGTTACACGGATATGTATTTCCTGGTCTGATATACCTGTTTTCGAAACGAGTGC	1139
DB	1080		
QY	1080	CATACATGGTTACACGGATATGTATTTCCTGGTCTGATATACCTGTTTTCGAAACGAGTGC	1140
DB	1080		
QY	1140	CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTT	1199
DB	1140		
QY	1140	CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTT	1199
DB	1140		
QY	1200	TGTTGTTTTGGTTGGAAGTAATCAATAGTGAATCTAGSACAGGTTTCGGGGTAAAGTACC	1259
DB	1200		
QY	1200	TGTTGTTTTGGTTGGAAGTAATCAATAGTGAAGTCAAGAACAGGTTTGGTGAAGTAAAC	1260
DB	1200		
QY	1260	GGGAGTGTAGAGAAAGGCTGGGTTATGTTATGGCGGAGGAGTACTGTTACATAGGGGT	1319
DB	1260		
QY	1260	GGGAGTGTAGAGAAAGGCTGGGTTATGTTATGGCGGAGGAGTACTGTTACATAGGGGT	1319
DB	1260		
QY	1320	CATAGGTGAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCACTGAGC	1379
DB	1320		
QY	1320	CATAGGTGAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCACTGAGC	1379
DB	1320		
QY	1380	CCACTCCCCCTGACCCCTGGGTGATCGGGGACGAGGCGCAAAATTAACCTTAACCTTTC	1439
DB	1380		
QY	1380	CCACTCCCCCTGACCCCTGGGTGATCGGGGACGAGGCGCAAAATTAACCTTAACCTTTC	1439
DB	1380		
QY	1440	TTATTCTGTAGTATTCAAAGGGCACAGACGGGGGTTTGACCCCTCTCGGGGGAAGAA	1499
DB	1440		
QY	1440	TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCGGGGGAACAA	1500
DB	1440		
QY	1500	AGTCATTAATATGAAATCTCATGTCCACCGCCAGAGGGCGTCTGACTCTGGTTC	1559
DB	1500		
QY	1500	AGTCATTAATATGAAATCTCATGTCCACCGCCAGAGGGCGTCTGACTCTGGTTC	1559
DB	1500		
QY	1560	GCTTGACAGTATATCCGAAGTTCGGGAGAGGCGGGTGTGAGATGCAATTTTTTCCTTC	1619
DB	1560		
QY	1560	GCTTGACAGTATATCCGAAGTTCGGGAGAGGCGGGTGTGAGATGCAATTTTTTCCTTC	1619
DB	1560		
QY	1620	TCACGCGGTAAACGGTGGCGGGGTGACACGACGAGGCGCGGAGGAGTCTGGGCCAA	1679
DB	1620		

[illegible]

421	Db	 GTACCTTGTGGAGACGGGAATTCGTGTCACCGTTGCAAGACAGCACCCCTGTAAACGTTTG	480
481	Qy	TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGCTGAGCGGAAAAATTCAGAAAGCGTGG	540
481	Db	TCAAAATTTCCGCGGCTGGCTGAACTTTTGAAGCTGAGCGGAAAAATTCGAAGCGTGG	540
541	Qy	ATTGGAGACTAATGTACACGTCATTGTGGGCCACCTCGGTGTGTGTAAAGCAAAATGGG	600
541	Db	ATTGGAAAAACAATGTACACTTCATTGTGGGCCACCTCGGTGTGTGTAAAGCAAAATGGG	600
601	Qy	CTGCTAATTTTCAGACCCCGGAAAAACACATACTGGAAAAACCACTAGAAAAACAAGTGGTGGG	660
601	Db	CTGCTAATTTTCAGAACCCCGGAAAAACCACTCTGGAAAAACCACTAAAAACAAGTGGTGGG	660
661	Qy	ATGGTTACCATGTGTGAAGAAGTGGTTTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
661	Db	ATGGTTACCATGTGTGAAGAAGTGGTTTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
721	Qy	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTGAGACTAAAGGTGGAACTG	780
721	Db	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTGAAAACTAAAGGTGGAACTG	780
781	Qy	TACCTTTTTTGGCCCGCAGTATTCTGATTCACAGCAATCAGACCCCGTTGGAAATGCTACT	840
781	Db	TACCTTTTTTGGCCCGCAGTATTCTGATTCACAGCAATCAGACCCCGTTGGAAATGCTACT	840
841	Qy	CCTCAACTGCTGCCAGCTGTAGAAGCTCTTTTATCGGAGGATTACTTCTCTTGTTATTTT	900
841	Db	CCTCAACTGCTGCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCTCTTGTTATTTT	900
901	Qy	GGAGAAATGCTACAGAAACAATCCACGGAGGAAGGGGCCAGTTGCTCACCCCTTCCCCCC	960
901	Db	GGAGAAATGCTACAAACAATCCACGGAGGAAGGGGCCAGTTGCTCACCCCTTCCCCCC	960
961	Qy	CATGCCCTGAATTTCCATATGAAATAAATTAATCTAGTCTTTTTTTTATCACTTCGTAATGGT	1020
961	Db	CATGCCCTGAATTTCCATATGAAATAAATTAATCTAGTCTTTTTTTTATCACTTCGTAATGGT	1020
1021	Qy	TTTTTATTATTCATTAAAGGTTT-AGTGGGGGTCTTTTAAATTAATTTCTCTCAATTGTA	1079
1021	Db	TTTTTATTATTCATTAAAGGTTTCAAGTGGGGGTCCTTAAAGATTAAATTTCTCTCAATTGTA	1080
1080	Qy	CATACATGGTTACACGGATATGTATTCTCTGGTCGTATATACCTGTTTTCGAAACGCACTGC	1139
1081	Db	CATACATGGTTACACGGATATGTAGTCTCTGTCGTATTTACTGTTTTCGAAACGCACTGC	1140
1140	Qy	CGAGGCTCAGTGGTCTPACATTTCCAGCAGTTGTAGTCTCAGCCACAGCTGTTTCTTTT	1199
1141	Db	CGAGGCTCAGTGGTCCACATTTCCAGCAGTTGTAGCCTCAGCCAAAGCTGATTCCTTT	1200
1200	Qy	TGTTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGACAGGTTTGGGGTAAAGTACC	1259
1201	Db	TGTTATTTGGTTGGAAGTAATCAATAGTGAGATCAAGAACAGGTTTGGGTGTGAAGTAAC	1360
1260	Qy	GGGAGTGTAGAGAAAGGGCTGGGTATGGTATGGCGGAGGAGTAGTTTACATAGGGGT	1319
1261	Db	GGGAGTGTAGAGAAAGGGTTGGGGATTTGTATGGCGGGAGGAGTAGTTTACATAGGGT	1320
1320	Qy	CATAGGTGAGGCTGTGGCTTTGTTACAAAGTTTATCATCTAAATAACAGCACTGGAGC	1379
1321	Db	CATAGGTGAGGCTGTGGCTTTGTTACAAAGTTTATCATCTAAATAACAGCACTGGAGC	1380
1380	Qy	CCACTCCCTGTCAACCTGGGTGATCGGGAGCAGGGCCAGAAATTCACCTTAACCTTTC	1439
1381	Db	CCACTCCCTCATCAACCTGGGTGATGGGGAGCAGGCCAGAAATTCACCTTAACCTTTC	1440
1440	Qy	TTATTTCTGTAGTATTCAAAGGCGCACAGACGGGGGTTTGACCCCCCTCTCGGGGGAAGAA	1499
1441	Db	TTATTTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGGAACAA	1500
1500	Qy	AGTCATTAAATTTGAATCTCATATGCTCCACCGCCCGAGGAGGGGTTCTGACTGTGGTTC	1559

Db	1501	AGTCGTCAATTTTAAATCTCATGTCCACCGCCAGGAGGGCGTTGTGACTGTGGTAC	1560
Qy	1560	GCTTGACAGATATATCCGAAGGTGCGGAGAGCGGGGTGTTGAAGATGCCAATTTTTCCTTC	1619
Db	1561	GCTTGACAGATATATCCGAAGGTGCGGAGAGCGGGGTGTTGAAGATGCCAATTTTTCCTTC	1620
Qy	1620	TCCAGCGGTAAACGGTGGCGGGGTGGACGAGCCAGAGGGCGCGCGAGAGATCTGGGCCAA	1679
Db	1621	TCCAACGGTATACGGTGGCGGGGTGGACGAGCCAGAGGGCGCGCGAGAGATCTGGGCCAA	1680
Qy	1680	GATGGCTGCGGGGGCGGTGCTTCTTCTTCGGTAAACGCCCTCTTTGGATAGCTCATATCTG	1739
Db	1681	GATGGCTGCGGGGGCGGTGCTTCTTCTTCGGTAAACGCCCTCTTTGGATAGCTCATATCTG	1740
Qy	1740	AAAAACGAAAGATGCGCTGTAAAGTATT	1767
Db	1741	AAAAACGAAAGATGCGCTGTAAAGTATT	1768
RESULT 9			
US-10-653-849-1			
; Sequence 1, Application US/10653849			
; Publication No. US20040132178A1			
; GENERAL INFORMATION:			
; APPLICANT: WANG, LI			
; APPLICANT: BABIUK, LORNE A.			
; APPLICANT: POTTER, ANDREW A.			
; APPLICANT: WILLSON, PHILIP			
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM			
; TITLE OF INVENTION: PIGS			
; FILE REFERENCE: 9000-0040			
; CURRENT APPLICATION NUMBER: US/10/653,849			
; CURRENT FILING DATE: 2003-09-02			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/209,961			
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233			
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750			
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16			
; NUMBER OF SEQ ID NOS: 24			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 1768			
; TYPE: DNA			
; ORGANISM: Porcine Circovirus Type II			
US-10-653-849-1			
Query Match 92.2%; Score 1629.6; DB 17; Length 1768;			
Best Local Similarity 95.5%; Pred. No. 0;			
Matches 1688; Conservative 0; Mismatches 79; Indels 1; Gaps 1			
Qy	1	ACCAGCGCACTTCGGCAGCGGAGCAGCACTTCGGCAGCAGCACTTCAGCAGCAACATGCCCGCA	60
Db	1	ACCAGCGCACTTCGGCAGCGGAGCAGCACTTCGGCAGCAGCACTTCAGCAGCAACATGCCCGCA	60
Qy	61	AGAAGAATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTGTTCACTCTGTAATAATC	120
Db	61	AGAAGAATGGAAGAGCGGACCCCAACCCCAACACATAAAGTGGGTGTTCACTCTGTAATAATC	120
Qy	121	CTTCCGAAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTTTCGATTATTTTA	180
Db	121	CTTCCGAAGACGAGCGGCAAGAAATACGGGAGCTCCCAATCTCCCTATTTTCGATTATTTTA	180
Qy	181	TTGTTGGCGAGGAGGTTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGTAATT	240
Db	181	TTGTTGGCGAGGAGGTTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGTAATT	240
Qy	241	TTGTGAAGAACGAGACTTTTTAATAAGTGAAGTGGTATTTGGGTCCCGCTGCCACATCG	300
Db	241	TTGTGAAGAACGAGACTTTTTAATAAGTGAAGTGGTATTTGGGTCCCGCTGCCACATCG	300
Qy	301	AGAAACGGAAGGAACAGATCAGCAGAGATAAAGATATCTGCAGTAAGAGCAACTTAC	360

121 QY CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATTTTAA 180
121 Db CTTCCGAAGACGAGCGCAAGAAATACGGGAGCTCCCAATCTCCCTATTTGATTTTAA 180
181 QY TTGTTGGCGAGGAGGTAAATGAGGAAGAGCAACACCTCCAGGGGTTCGCTAAAT 240
181 Db TTGTTGGCGAGGAGGTAAATGAGGAAGAGCAACACCTCCAGGGGTTCGCTAAAT 240
241 QY TTGTGAAGAACAGACATTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGTGCACATCG 300
241 Db TTGTGAAGAACAGACATTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGTGCACATCG 300
301 QY AGAAGCGAAGGACAGATCAGCAGATAAAGATATCTGAGTAAAGAGGCAACTTAC 360
301 Db AGAAGCGAAGGACAGATCAGCAGATAAAGATATCTGAGTAAAGAGGCAACTTAC 360
361 QY TGATGGAGTGGAGCTCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTCTGTGA 420
361 Db TTATTGAATGTGAGCTCTCTGATCTCAAGGACCAACCGAGTGACCTGTCTACTCTGTGA 420
421 QY GTACCTTGTGGAGACGGGAGTCTGTGACCGTTGACAGACGACCTGTAAAGCTTTG 480
421 Db GTACCTTGTGGAGACGGGAGTCTGTGACCGTTGACAGACGACCTGTAAAGCTTTG 480
481 QY TCAGAAATTTCCGCGGGTGGTGAACCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
481 Db TCAGAAATTTCCGCGGGTGGTGAACCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
541 QY ATTGAAGACTAATGTACACGTCATTTGTGGGCGCACCTGGGTGTGTTAAAGCAAAATGG 600
541 Db ATTGAAGACTAATGTACACGTCATTTGTGGGCGCACCTGGGTGTGTTAAAGCAAAATGG 600
601 QY CTGCTAAATTTTGCAGACCGGAAACACATCTGGAACACCTGGAACCAAGTGGTGG 660
601 Db CTGCTAAATTTTGCAGACCGGAAACACATCTGGAACACCTGGAACCAAGTGGTGG 660
661 QY ATGGTTACCTGCTGAGAGGAGTGTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 720
661 Db ATGGTTACCTGCTGAGAGGAGTGTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 720
721 QY ATGATCTACTGAGACTGTGTGATCGATATCCATTCGATGTAGAGCTAAAGTGGAATG 780
721 Db ATGATCTACTGAGACTGTGTGATCGATATCCATTCGATGTAGAGCTAAAGTGGAATG 780
781 QY TACCTTTTGGCGCGCAGTATTCGATTAACGCAATCAGACCCCGTGGATGGTACT 840
781 Db TACCTTTTGGCGCGCAGTATTCGATTAACGCAATCAGACCCCGTGGATGGTACT 840
841 QY CCTCAACTGCTGCTCCAGCTGTAGAGCTCTATCGGAGGATTAATCTCTTGGTATTT 900
841 Db CCTCAACTGCTGCTCCAGCTGTAGAGCTCTATCGGAGGATTAATCTCTTGGTATTT 900
901 QY GGAAGAACTGACAGAACCAATCCAGGAGGAGGGGCGAGTTCGTCACCTTTCCCTCC 960
901 Db GGAAGAACTGACAGAACCAATCCAGGAGGAGGGGCGAGTTCGTCACCTTTCCCTCC 960
961 QY CATGCCCTGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
961 Db CATGCCCTGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
1021 QY TTTTATTATTCAATAAGGG-TTAAGTGGGGGTCTTTTAAATTAATTAATTAATTAATTA 1079
1021 Db TTTTATTATTCAATAAGGG-TTAAGTGGGGGTCTTTTAAATTAATTAATTAATTAATTA 1080
1080 QY CATACTAGTTACCGGATTTGATTTCTGCTGCTGATATATCTGTTTTCGAGCGAGTGC 1139
1080 Db CATACTAGTTACCGGATTTGATTTCTGCTGCTGATATATCTGTTTTCGAGCGAGTGC 1140
1140 QY CGAGGCTAGTGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTT 1199
1140 Db CGAGGCTAGTGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTT 1200
1200 QY TGTGTTTGTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC 1259

1201 Db TGTATTTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAA 1260
1260 QY GGGAGTGTAGAGAGGCGTGGTTATGTTATGCGGGAGGAGTAGTTTACATAGGGGT 1319
1261 Db GGGAGTGTAGAGAGGCGTGGTTATGTTATGCGGGAGGAGTAGTTTACATATGGT 1320
1320 QY CATAGTGAAGGCTGTGGCTTTTGTACAAAGTTATCATCTTAAATAACAGCAGTGGAGC 1379
1321 Db CATAGTGAAGGCTGTGGCTTTTGTACAAAGTTATCATCTTAAATAACAGCAGTGGAGC 1380
1380 QY CCACTCCCCTGTCAACCTGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAA 1439
1381 Db CCACTCCCCTGTCAACCTGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAA 1440
1440 QY TTATTTCTGTAGTATTTCAAAAGGCGACAGCGGGGTTTGAACCCCTCTCTGGGGGAAGAA 1499
1441 Db TTATTTCTGTAGTATTTCAAAAGGCGATAGAAATTTTGTGTCTCCCTCCCGGGGAACAA 1500
1500 QY AGTCATTAATATTTGAATCTCATCATGTCCACCGCCAGAGGGCGTTCTGACTGTGGTTC 1559
1501 Db AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCAGAGGGCGTTGTGACTGTGGTAC 1560
1560 QY GCTTGACAGTATATCCGAAGGTCGGGAGAGGGGCTGTGAAGATGCCATTTTCTTTC 1619
1561 Db GCTTGACAGTATATCCGAAGGTCGGGAGAGGGGCTGTGAAGATGCCATTTTCTTTC 1620
1620 QY TCCAGCGGTAAACGTCGGCGGGTGAACGAGCCAGCGGGCGGGCGGAGGATCTGCCCAA 1679
1621 Db TCCAGCGGTAAACGTCGGCGGGTGAACGAGCCAGCGGGCGGGCGGAGGATCTGCCCAA 1680
1680 QY GATGGCTGCGGGGCGGTGTCTTCTTCTGCGGTAAACGCTCTCTTGGATAGTATCTG 1739
1681 Db GATGGCTGCGGGGCGGTGTCTTCTTCTGCGGTAAACGCTCTCTTGGATAGTATCTG 1740
1740 QY AAAACGAAGAGTGGCTGTAAATTT 1767
1741 Db AAAACGAAGAGTGGCTGTAAATTT 1768

RESULT 12
US-10-653-849-11
; Sequence 11, Application US/10653849
; Publication No. US20040132178A1
; GENERAL INFORMATION:
; APPLICANT: WANG, LI
; APPLICANT: BABIUK, LORNE A.
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: WILLSON, PHILIP
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
; FILE REFERENCE: 9000-0040
; CURRENT APPLICATION NUMBER: US/10/653,849
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/209,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine Circovirus Type II
US-10-653-849-11

Query Match 92.1%; Score 1628; DB 17; Length 1768;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1687; Conservative 0; Mismatches 80; Indels 1; Gaps 1;
QY 1 ACCAGCGCACTTGGCGAGCGGAGCACCTCGGAGCACCTCAGCAGCAATGCCAGCA 60

Db 1 ACCAGCGCACTTCGCGAGCGGAGCACCTCGCGAGCACCTCAGCAGCAACATGCCAGCA 60
Qy 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTCTCACTCTGTAATATC 120
Db 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTCTCACTCTGTAATATC 120
Qy 121 CTTCGGAAGAGCGGCAAGAAATACCGGATCTTCCAAATATCCCTATTTGATTTTA 180
Db 121 CTTCGGAAGAGCGGCAAGAAATACCGGATCTTCCAAATATCCCTATTTGATTTTA 180
Qy 181 TTGTTGGCGAGGATTAATGAGGAAGCAAGCAACCTCACTCAGGGGTTCGTAATTT 240
Db 181 TTGTTGGCGAGGATTAATGAGGAAGCAAGCAACCTCACTCAGGGGTTCGTAATTT 240
Qy 241 TTGTCGAAGAGGACTTTTAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Db 241 TTGTCGAAGAGGACTTTTAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Qy 301 AGAAGCGAAAGGAACAGATCAGCAAGATAAAGATACTGCAAGTAAAGAGGCAACTTAC 360
Db 301 AGAAGCGAAAGGAACAGATCAGCAAGATAAAGATACTGCAAGTAAAGAGGCAACTTAC 360
Qy 361 TGAAGAGTGGAGCTCCTAGATCTCAGGGAACAACGAGTGAACCTGTCTACTGTGTA 420
Db 361 TTAATTAATGTGGAGCTCCTAGATCTCAGGGAACAACGAGTGAACCTGTCTACTGTGTA 420
Qy 421 GTACCTTTGAGAGCGGGAGTCTGAGTCCGTTGCAAGCAGCAGCACCCTGTAACGTTG 480
Db 421 GTACCTTTGAGAGCGGGAGTCTGAGTCCGTTGCAAGCAGCAGCACCCTGTAACGTTG 480
Qy 481 TCAGAAATTTCCGCGGCTGGCTGAATTTTGAAGTGAAGGGAATGCAAGAGCGTG 540
Db 481 TCAGAAATTTCCGCGGCTGGCTGAATTTTGAAGTGAAGGGAATGCAAGAGCGTG 540
Qy 541 ATTGGAAGACTAATGTACAGTCTATTGTTGGGCCACCTGGGTGGTAAAGCAATGGG 600
Db 541 ATTGGAAGACTAATGTACAGTCTATTGTTGGGCCACCTGGGTGGTAAAGCAATGGG 600
Qy 601 CTGCTAATTTTGCAGACCGGAAACCAATATCTGAAACCACTAGAACAGTGGTGG 660
Db 601 CTGCTAATTTTGCAGACCGGAAACCAATATCTGAAACCACTAGAACAGTGGTGG 660
Qy 661 ATGGTTACCATGTAAGAGTGGTTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Db 661 ATGGTTACCATGTAAGAGTGGTTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAATG 780
Db 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAATG 780
Qy 781 TACCTTTTGGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
Db 781 TACCTTTTGGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
Qy 841 CCTCAACTGCTGCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900
Db 841 CCTCAACTGCTGCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900
Qy 901 GGAAGAAATGCTACAGAAACAATCCACGAGGAAGGGGCCAGTTCGTACCCCTTTCCCCC 960
Db 901 GGAAGAAATGCTACAGAAACAATCCACGAGGAAGGGGCCAGTTCGTACCCCTTTCCCCC 960
Qy 961 CATGCCCTGAATTCATATGAATAAATTAATGAGTCTTTTATCACTTGTATGTT 1020
Db 961 CATGCCCTGAATTCATATGAATAAATTAATGAGTCTTTTATCACTTGTATGTT 1020
Qy 1021 TTTTATTTATTAAGG-TTAAAGTGGGGTCTTTAAATTAATTTCTCTGAAATGTA 1079
Db 1021 TTTTATTTATTAAGG-TTAAAGTGGGGTCTTTAAATTAATTTCTCTGAAATGTA 1080
Qy 1080 CATACATGGTTACCGATATTTGATTTCTTGGTGGTATATCTGTTTTCGAAACGAGTGC 1139

Db 1081 CATACATGGTTACCGATATTTGATTCCTGGTCTGATTTACTCTTTTCGAACGAGTGC 1140
Qy 1140 CGAGCCCTACGTGTCTACATTTCCACAGATTTTGTAGTCTCAGCAACAGCTGGTTCTTT 1199
Db 1141 CGAGCCCTACGTGTCTACATTTCCACAGATTTTGTAGTCTCAGCAACAGCTGGTTCTTT 1200
Qy 1200 TGTGTTTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC 1259
Db 1201 TGTATTATTGGTTGGAAGTAAATCAATAGTGAAGTCAAGAACAGGTTTGGGTGGAAGTAA 1260
Qy 1260 GGGAGTGTAGCAAGGGCTGGGTATGTTATGGCGGAGGAGTAGTTTACATAGGGGT 1319
Db 1261 GGGAGTGTAGCAAGGGGTGGGGATTTGTTATGGCGGAGGAGTAGTTTACATATGGT 1320
Qy 1320 CATAGGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCATGGAGC 1379
Db 1321 CATAGGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCATGGAGC 1380
Qy 1380 CCACCTCCCTGTACCCCTGGGTGATCGGGAGGAGGCGCAGANTTCAACCTTAACCTTTC 1439
Db 1381 CCACCTCCCTATACCCCTGGGTGATGGGGAGGAGGCGCAGAAATTCACCTTAACTTTTC 1440
Qy 1440 TTATTCTGTAGTATTCAAAGGGCAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAA 1499
Db 1441 TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGGTCCCCCTCCCGGGGAACAA 1500
Qy 1500 AGTCATTAATATTGAATCTCATGTCCACCGCCAGGAGGGGCTTCTGACTGTGGTTC 1559
Db 1501 AGTCATTAATTTTAAATCTCATGTCCACCGCCAGGAGGGCTTCTGACTGTGGTAC 1560
Qy 1560 GCTTGACAGTATATCCGAAGGTGGGGAGAGCGGGTGTGAGAGTCCATTTTTCCTTC 1619
Db 1561 GCTTGACAGTATATCCGAAGGTGGGGAGAGCGGGTGTGAGAGTCCATTTTTCCTTC 1620
Qy 1620 TCCAGCGGTACGGTGGCGGGTGGAGCGAGCGGGCGGGCGGAGGATCTGGCCCAA 1679
Db 1621 TCCAGCGGTACGGTGGCGGGTGGAGCGAGCGGGCGGGCGGAGGATCTGGCCCAA 1680
Qy 1680 GATGCTCGGGGGCGGTGTCTTCTTTCGGTAAACGCTCTCTGGATACGTCATATCTG 1739
Db 1681 GATGCTCGGGGGCGGTGTCTTCTTCTCGGTAAACGCTCTCTGGATACGTCATATCTG 1740
Qy 1740 AAAACGAAGAAGTGGCTGTAAAGTATT 1767
Db 1741 AAAACGAAGAAGTGGCTGTAAAGTATT 1768

RESULT 13
US-10-112-540-1
; Sequence 1, Application US/10112540
; Publication No. US20020177216A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; APPLICANT: Tikoo, Suresh K.
; APPLICANT: Willson, Philip
; APPLICANT: Babiuk, Lorne A.
; TITLE OF INVENTION: METHODS TO CULTURE CIRCOVIRUS
; FILE REFERENCE: 293102003100
; CURRENT APPLICATION NUMBER: US/10/112,540
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/279,173
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-10-112-540-1

Query Match 91.7%; Score 1620; DB 13; Length 1768;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1682; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 1 ACCAGCGCATTTCGGCAGCGCAGCACCTCGGAGCAGCCTCAGCAGCAACATGCCCCAGCA 60
Db 1 ACCAGCGCATTTCGGCAGCGCAGCACCTCGGAGCAGCCTCAGCAGCAACATGCCCCAGCA 60
QY 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAAGGTGGGTCTCACTCTGAATAATC 120
Db 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAAGGTGGGTCTCACTCTGAATAATC 120
QY 121 CTTCCGAAGACGAGCGGCAAGAAATACCGGATCTCCAAATCTCCCTATTTGATTTTAA 180
Db 121 CTTCCGAAGACGAGCGGCAAGAAATACCGGATCTCCAAATCTCCCTATTTGATTTTAA 180
QY 181 TTGTTGGCGAGGAGGTAATCAGGAAGCAACACCTCACCTCAGGGGTTCCTTAAT 240
Db 181 TTGTTGGCGAGGAGGTAATCAGGAAGCAACACCTCACCTCAGGGGTTCCTTAAT 240
QY 241 TTGTGAAGACGACATTTTAAATGAAGTGAAGTGAATTTGGGTGCCCGTGCACATCG 300
Db 241 TTGTGAAGACGACATTTTAAATGAAGTGAAGTGAATTTGGGTGCCCGTGCACATCG 300
QY 301 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCAACTTAC 360
Db 301 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCAACTTAC 360
QY 361 TGATGGAGTGTGGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGCTGTA 420
Db 361 TTATGAAATGAGAGCTCTCGATCTCAGGACCAACGAGTGACCTGTCTACTGCTGTA 420
QY 421 GTACCTTGTGGAGCGGGAGTGTGTGAACGTTGACAGAGCAGCACCTGTAAAGTTTG 480
Db 421 GTACCTTGTGGAGCGGGAGTGTGTGAACGTTGACAGAGCAGCACCTGTAAAGTTTG 480
QY 481 TCAGAAATTCGCGGGTGGCTGAACCTTTGAAAGTGAAGGAGGGAATCAGAGCGTG 540
Db 481 TCAGAAATTCGCGGGTGGCTGAACCTTTGAAAGTGAAGGAGGGAATCAGAGCGTG 540
QY 541 ATTGAAGACTAATGTACACGTCATTGTGGGCGCACCTGGGTGTGTTAAAGCAAAATGGG 600
Db 541 ATTGAAGACTAATGTACACGTCATTGTGGGCGCACCTGGGTGTGTTAAAGCAAAATGGG 600
QY 601 CTGCTAAATTTTCAGACCGGGAACACATATCGAAACACCTAGAAACCAAGTGGTGGG 660
Db 601 CTGCTAAATTTTCAGACCGGGAACACATATCGAAACACCTAGAAACCAAGTGGTGGG 660
QY 661 ATGTTTACCATGGTGAAGAGTGGTGTATTTGATGACCTTTATGGCTGGCTGCCCTGG 720
Db 661 ATGTTTACCATGGTGAAGAGTGGTGTATTTGATGACCTTTATGGCTGGCTGCCCTGG 720
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCAGTGTAGAGCTAAAGGTGGAACGTG 780
Db 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCAGTGTAGAGCTAAAGGTGGAACGTG 780
QY 781 TACCTTTTTCGCGCAGTATCTGATTAACAGCAATCAGACCCGTTGGAATGGTACT 840
Db 781 TACCTTTTTCGCGCAGTATCTGATTAACAGCAATCAGACCCGTTGGAATGGTACT 840
QY 841 CTTCAACTCTCTCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTGTTGATTTT 900
Db 841 CTTCAACTCTCTCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTGTTGATTTT 900
QY 901 GGAAGAAATCTCAGAAACATCAGCGAGGAAGGGGCGAGTTCGTACCCCTTCCCCC 960
Db 901 GGAAGAAATCTCAGAAACATCAGCGAGGAAGGGGCGAGTTCGTACCCCTTCCCCC 960
QY 961 CATGCCCTGAATTTCCATATGAATAAATATCTAGTCTTTTTTATCACTTGGTAATGT 1020
Db 961 CATGCCCTGAATTTCCATATGAATAAATATCTAGTCTTTTTTATCACTTGGTAATGT 1020
QY 1021 TTTTATTTTCAATAGGG-TTAAGTGGGGGTCTTTAAATTAATTTCTCTGAATGTA 1079
Db 1021 TTTTATTTTCAATTTAGGGTTAAGTGGGGGTCTTTAAAGATTAAATTTCTCTGAATGTA 1080

QY 1080 CATACATGTTTACCGGATATTGTATTCCTGTGCTATATCTATCTGTTTTCGAACGAGTGC 1139
Db 1081 CATACATGTTTACCGGATATTGTATTCCTGTGCTATATCTATCTGTTTTCGAACGAGTGC 1140
QY 1140 CGAGGCTACGTTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTCTTT 1199
Db 1141 CGAGGCTACGTTCTACATTTCTAGAGTTTGTAGCTTACCCCAAGCTGATTCCTTT 1200
QY 1200 TGTGTTTGTGTTGCAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC 1259
Db 1201 TGTATTTGTGTTGCAAGTAAATCAATAGTGAATCAAGACAGGTTTGGGTGTGAAGTAA 1260
QY 1260 GGAGTGTAGGAGAAAGGCTGGGTATATGATGCGGGAGGAGTAGTTTACATAGGGT 1319
Db 1261 GGAGTGTAGGAGAAAGGCTGGGGATTTGATGCGGGAGGAGTAGTTTACATATGGT 1320
QY 1320 CATAGTGTAGGCTGTGGCTTTTGTACAAAGTTTATCATCTAGAAATAACAGCACTGGAGC 1379
Db 1321 CATAGTGTAGGCTGTGGCTTTTGTACAAAGTTTATCATCTAGAAATAACAGCACTGGAGC 1380
QY 1380 CCACTCCCTGTCAACCTGGGTGATCGGGAGCAGGCGCCAGAAATTTCAACCTTAACTTTTC 1439
Db 1381 CCACTCCCTGTCAACCTGGGTGATCGGGAGCAGGCGCCAGAAATTTCAACCTTAACTTTTC 1440
QY 1440 TTATTTGTAGTATTTCAAGGGCAGAGCGGGGTTTGACCCCTCTCTGGGGGAGAA 1499
Db 1441 TTATTTGTAGTATTTCAAGGGGATAGAGATTTTGTGGTCCCCCTCCCGGGGAGAA 1500
QY 1500 AGTCAATTAATTTGAATCTCATCTCATGTCACCGCCAGGAGGGGTTTCACTGTGGTTC 1559
Db 1501 AGTCAATTAATTTGAATCTCATCTCATGTCACCGCCAGGAGGGGTTTCACTGTGGTTC 1560
QY 1560 GCTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTTCCTTC 1619
Db 1561 CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTTCCTTC 1620
QY 1620 TCCAGCGGTAAAGTGGCGGGGTGAGCAGACCAAGCGGCGCGGAGGATCTGGCCAA 1679
Db 1621 TCCAAAGGTAGCGGTGGCGGGGTGAGCAGACCAAGCGGCGCGGAGGATCTGGCCAA 1680
QY 1680 GATGGCTCGGGGCGGTGCTCTCTTCGTTAAACCCCTCTTGGATAGCTCATATCTG 1739
Db 1681 GATGGCTCGGGGCGGTGCTCTCTTCGTTAAACCCCTCTTGGATAGCTCATATCTG 1740
QY 1740 AAAACGAAGAAGTGCCTGTAAAGTATT 1767
Db 1741 AAAACGAAGAAGTGCCTGTAAAGTATT 1768

RESULT 14

US-09-784-962-1
; Sequence 1, Application US/09784962
; Patent No. US20020146431A1
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon M.
; APPLICANT: MEEHAN, Brian M.
; APPLICANT: ELLIS, John A.
; APPLICANT: KRAKOWKA, George S.
; APPLICANT: AUDONNET, Jean-Christophe F.
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE
; FILE REFERENCE: 454313-2338
; CURRENT APPLICATION NUMBER: US/09/784,962
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/347,594
; PRIOR FILING DATE: 1999-07-04
; PRIOR APPLICATION NUMBER: 98 08777
; PRIOR FILING DATE: 1998-07-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus

US-09-784-962-1

Query Match 79.9%; Score 1412; DB 9; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGCGAGCGGAGCACTCGGAGCACCTCGGAGCACCTCGAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGCGAGCGGAGCACTCGGAGCACCTCGAGCAACATGCCAGCA 407

QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGAATATC 120
DB 408 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGAATATC 467

QY 121 CTTCCGAGAGCAGCGGAGCAAAATACGGATCTTCCAATATCCCTATTGATATTTA 180
DB 468 CTTCCGAGAGCAGCGGAGCAAAATACGGATCTTCCAATATCCCTATTGATATTTA 527

QY 181 TTGTTGGCGAGGAGGTAAAGGAGGAGCAACACCTCACCTCCAGGGTTTCGTAAT 240
DB 528 TTGTTGGCGAGGAGGTAAAGGAGGAGCAACACCTCACCTCCAGGGTTTCGTAAT 587

QY 241 TTGGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGGTGCCCGCTCCCAATCG 300
DB 588 TTGGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGGTGCCCGCTCCCAATCG 647

QY 301 AGAAGCGAAGAGCAGATCAGCAGATAAAGATCTGCAGTAAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGAGCAGATCAGCAGATAAAGATCTGCAGTAAAGAGGCAACTTAC 707

QY 361 TGAATGAGTGTGAGCTCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTGTGTA 420
DB 708 TGAATGAGTGTGAGCTCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTGTGTA 767

QY 421 GTACCTTGTGAGAGCGGAGTGTGTGACCGTGTGAGAGCAGACCCCTGTAAAGTTG 480
DB 768 GTACCTTGTGAGAGCGGAGTGTGTGACCGTGTGAGAGCAGACCCCTGTAAAGTTG 827

QY 481 TCAGAAATTCGCGGGCTGGCTGAATTTGAAAGTGAAGGAGGAAATGCAGAGCGTG 540
DB 828 TCAGAAATTCGCGGGCTGGCTGAATTTGAAAGTGAAGGAGGAAATGCAGAGCGTG 887

QY 541 ATTGGAAGACTAATGTACACGCTATTGTGGGGCCACTGGGTGTGTTAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACACGCTATTGTGGGGCCACTGGGTGTGTTAAAGCAATGGG 947

QY 601 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACCACTAGAAAACAAGTGTGGG 660
DB 948 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACCACTAGAAAACAAGTGTGGG 1007

QY 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 720
DB 1008 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 1067

QY 721 ATGATCTACTGACACTGTGTGATTCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 780
DB 1068 ATGATCTACTGACACTGTGTGATTCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 1127

QY 781 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGTACT 840
DB 1128 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGTACT 1187

QY 841 CCTCAACTGTGTCCAGCTGTGAGAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 900
DB 1188 CCTCAACTGTGTCCAGCTGTGAGAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 1247

QY 901 GGAAGATGCTACAGAACCAATCCACGAGGAGGCGGCGAGTTTCGTCACCTTTCCCGCC 960
DB 1248 GGAAGATGCTACAGAACCAATCCACGAGGAGGCGGCGAGTTTCGTCACCTTTCCCGCC 1307

QY 961 CATGCCCTGAATTTTCAATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGGT 1020
DB 1308 CATGCCCTGAATTTTCAATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGGT 1367

QY 1021 TTTTATTATTATTAAGGTTAAAGTGGGGGTCTTTTAAATTAATTTCTCTGAATTTGAC 1080
DB 1368 TTTTATTATTATTAAGGTTAAAGTGGGGGTCTTTTAAATTAATTTCTCTGAATTTGAC 1427

QY 1081 ATACATGGTTACAGGATATTTCTGTCGTCTATATCTGTTTTCGAACGCAAGTCC 1140
DB 1428 ATACATGGTTACAGGATATTTCTGTCGTCTATATCTGTTTTCGAACGCAAGTCC 1487

QY 1141 GAGGCTACGTTGTTCTACATTTCCAGAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
DB 1488 GAGGCTACGTTGTTCTACATTTCCAGAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1547

QY 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGTTTGGGGGTAAAGTACCG 1260
DB 1548 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGTTTGGGGGTAAAGTACCG 1607

QY 1261 CGAGTGTGAGAGGCGTGGGTATGGTATGGGAGGAGTAGTTTACATAGGGTTC 1320
DB 1608 CGAGTGTGAGAGGCGTGGGTATGGTATGGGAGGAGTAGTTTACATAGGGTTC 1667

QY 1321 ATAGTGAAGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGAGGCC 1380
DB 1668 ATAGTGAAGGCTGTGGCTTTGTTTACAAAGTTATCATCTAGATAACAGCACTGAGGCC 1727

QY 1381 CACTCCCTGTCAACCTCGGTTGATCGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTGTCAACCTCGGTTGATCGGGAGCAGGGCCAG 1767

RESULT 15
US-09-884-514-1
; Sequence 1, Application US/09884514
; Patent No. US20020146432A1
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: CHARREIRE, John
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeilly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-1

Query Match 79.9%; Score 1412; DB 9; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGCGAGCGGAGCACTCGGAGCACCTCGGAGCACCTCGAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGCGAGCGGAGCACTCGGAGCACCTCGGAGCACCTCGAGCAACATGCCAGCA 407

QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGAATATC 120
DB 408 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGAATATC 467

QY 121 CTTCCGAGAGCAGCGGAGCAAAATACGGATCTTCCAATATCCCTATTGATATTTA 180
DB 468 CTTCCGAGAGCAGCGGAGCAAAATACGGATCTTCCAATATCCCTATTGATATTTA 527

QY 181 TTGTTGGCGAGGAGGTAAAGGAGGAGCAACACCTCACCTCCAGGGTTTCGTAAT 240
DB 528 TTGTTGGCGAGGAGGTAAAGGAGGAGCAACACCTCACCTCCAGGGTTTCGTAAT 587

QY 241 TTGGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGGTGCCCGCTCCCAATCG 300
DB 588 TTGGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGGTGCCCGCTCCCAATCG 647

QY 301 AGAAGCGAAGAGCAGATCAGCAGATAAAGATCTGCAGTAAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGAGCAGATCAGCAGATAAAGATCTGCAGTAAAGAGGCAACTTAC 707

QY 361 TGAATGAGTGTGAGCTCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTGTGTA 420
DB 708 TGAATGAGTGTGAGCTCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTGTGTA 767

QY 421 GTACCTTGTGAGAGCGGAGTGTGTGACCGTGTGAGAGCAGACCCCTGTAAAGTTG 480
DB 768 GTACCTTGTGAGAGCGGAGTGTGTGACCGTGTGAGAGCAGACCCCTGTAAAGTTG 827

QY 481 TCAGAAATTCGCGGGCTGGCTGAATTTGAAAGTGAAGGAGGAAATGCAGAGCGTG 540
DB 828 TCAGAAATTCGCGGGCTGGCTGAATTTGAAAGTGAAGGAGGAAATGCAGAGCGTG 887

QY 541 ATTGGAAGACTAATGTACACGCTATTGTGGGGCCACTGGGTGTGTTAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACACGCTATTGTGGGGCCACTGGGTGTGTTAAAGCAATGGG 947

QY 601 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACCACTAGAAAACAAGTGTGGG 660
DB 948 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACCACTAGAAAACAAGTGTGGG 1007

QY 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 720
DB 1008 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGG 1067

QY 721 ATGATCTACTGACACTGTGTGATTCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 780
DB 1068 ATGATCTACTGACACTGTGTGATTCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 1127

QY 781 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGTACT 840
DB 1128 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGTACT 1187

QY 841 CCTCAACTGTGTCCAGCTGTGAGAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 900
DB 1188 CCTCAACTGTGTCCAGCTGTGAGAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 1247

QY 901 GGAAGATGCTACAGAACCAATCCACGAGGAGGCGGCGAGTTTCGTCACCTTTCCCGCC 960
DB 1248 GGAAGATGCTACAGAACCAATCCACGAGGAGGCGGCGAGTTTCGTCACCTTTCCCGCC 1307

QY 961 CATGCCCTGAATTTTCAATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGGT 1020
DB 1308 CATGCCCTGAATTTTCAATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGGT 1367

Db 408 AGAAGATGGAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC 467
Qy 121 CTTCCGAAGACGAGCGCAAGAAAAATACCGGATCTTCCAAATATCCCTATTTGATTTTAA 180
Db 468 CTTCCGAAGACGAGCGCAAGAAAAATACCGGATCTTCCAAATATCCCTATTTGATTTTAA 527
Qy 181 TTGTTGGCGAGGAGGTAAATGAGAGGACCAACACCTCACCTCCAGGGTTCGCTAATT 240
Db 528 TTGTTGGCGAGGAGGTAAATGAGAGGACCAACACCTCACCTCCAGGGTTCGCTAATT 587
Qy 241 TTGTTGAGAACGACAGCTTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Db 588 TTGTTGAGAACGACAGCTTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 647
Qy 301 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATACTGCACTAAAGAGGCAACTTAC 360
Db 648 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATACTGCACTAAAGAGGCAACTTAC 707
Qy 361 TGATGGAGTGGAGCTCCTAGATCTCAGGACACGAGTGACCTGTACTCTCTGTA 420
Db 708 TGATGGAGTGGAGCTCCTAGATCTCAGGACACGAGTGACCTGTACTCTCTGTA 767
Qy 421 GTACCTCTGTGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCTCTGAACGTTG 480
Db 768 GTACCTCTGTGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCTCTGAACGTTG 827
Qy 481 TCAGAAATTTCCGCGGGTGGCTGAACCTTTTGAAGTGAAGCGGGAATGAGAGCGTG 540
Db 828 TCAGAAATTTCCGCGGGTGGCTGAACCTTTTGAAGTGAAGCGGGAATGAGAGCGTG 887
Qy 541 ATTGGAAGACTAATGTACACGTCATTTGTGGGCGCACCTGGGTGTGTAAGCAAAATGGG 600
Db 888 ATTGGAAGACTAATGTACACGTCATTTGTGGGCGCACCTGGGTGTGTAAGCAAAATGGG 947
Qy 601 CTGCTAAATTTGCAGACCGGAAACCAACATCTGGAACCACTAGAAACCAAGTGGTGGG 660
Db 948 CTGCTAAATTTGCAGACCGGAAACCAACATCTGGAACCACTAGAAACCAAGTGGTGGG 1007
Qy 661 ATGGTTACCATGGTGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Db 1008 ATGGTTACCATGGTGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067
Qy 721 ATGATCTACTGAGCTGTGTGATCGATATCCATTTGACTAGAGACTAAAGGTGGAACCTG 780
Db 1068 ATGATCTACTGAGCTGTGTGATCGATATCCATTTGACTAGAGACTAAAGGTGGAACCTG 1127
Qy 781 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
Db 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 1187
Qy 841 CCTCAACTGTGTCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900
Db 1188 CCTCAACTGTGTCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 1247
Qy 901 GGAAGATGCTACAGAACCAATCCAGGAGGAGGCGGCGAGTTCTGTCACCCCTTTCCCCCC 960
Db 1248 GGAAGATGCTACAGAACCAATCCAGGAGGAGGCGGCGAGTTCTGTCACCCCTTTCCCCCC 1307
Qy 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTTTATCACTTCGTAATGGT 1020
Db 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTTTATCACTTCGTAATGGT 1367
Qy 1021 TTTTATTTATTAAGGTTAAGTGGGGTCTTTTAAATTAATTAATCTCTGAATTTGTAC 1080
Db 1368 TTTTATTTATTAAGGTTAAGTGGGGTCTTTTAAATTAATTAATCTCTGAATTTGTAC 1427
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Db 1428 ATACATGTTTACAGGATATTTGATTTCTCGTGTATATATCTGTTTTTCGAACGAGTGCC 1487
Qy 1141 GAGGCTTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200
Db 1488 GAGGCTTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1547

Qy 1201 GTTGTGTTTGGTGGAAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
Db 1548 GTTGTGTTTGGTGGAAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGTAAAGTACCG 1607
Qy 1261 GGAGTGGTAGGAGAAAGGCTGGGTATGTTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1320
Db 1608 GGAGTGGTAGGAGAAAGGCTGGGTATGTTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1667
Qy 1321 ATAGGTGAGGCTGTGGCTTTTGTACAAAGTTATCTATAAAATAACAGCACTGGAGCC 1380
Db 1668 ATAGGTGAGGCTGTGGCTTTTGTACAAAGTTATCTATAAAATAACAGCACTGGAGCC 1727
Qy 1381 CACTCCCTGTGTCACTCCCTGGGTGATCGGGAGCAGGGCCAG 1420
Db 1728 CACTCCCTGTGTCACTCCCTGGGTGATCGGGAGCAGGGCCAG 1767

Search completed: December 8, 2004, 00:59:58
Job time : 934 secs

result No.	Score	Query Match	Length	DB	ID	Description	
C	1	48.2	2.7	1101	9	CNS00LT2	AL078714 Drosophil
	2	47.8	2.7	1101	9	CNS00LO0	AL068607 Drosophil
	3	46.6	2.6	661	6	CA297536	SCCSD1C0
C	4	46.6	2.6	922	9	CNS0073W	AL066784 Drosophil
	5	45.6	2.6	497	6	CA294389	CA294389 SCGLV101
	6	45.6	2.6	598	6	CA294459	SCSGLV101
C	7	45.6	2.6	667	6	CA108913	CA108913 SCSGHR106
	8	45.4	2.6	561	1	A1514058	A1514058 GH27112.5
	9	45.2	2.6	324	9	CE373054	CE373054 tigr-g8s-
C	10	45.2	2.6	1029	9	AG034053	AG034053 Pan trogl
	11	45	2.5	571	6	CA741621	CA741621 wialc.pk0
	12	45	2.5	603	6	CA103262	CA103262 SCEZHR104
C	13	45	2.5	622	6	CA300454	CA300454 SCSEFLV104
	14	45	2.5	640	6	CA198894	CA198894 SCSEFLV107
	15	45	2.5	721	6	CA104948	CA104948 SCJFHR1C0
C	16	45	2.5	1043	6	CA278752	SCCSD2D09
	17	44.8	2.5	560	6	CA227295	SCCSD2D09
	18	44.8	2.5	756	8	A2175609	SP_0132_A
C	19	44.6	2.5	816	6	CA066540	CEQAD101
	20	44.6	2.5	939	9	CNS00CNG	AL059400 Drosophil
	21	44.2	2.5	638	4	BI629442	BI629442 RH58310.5
C	22	44.2	2.5	946	6	CA103549	CA103549 SCEZHR108
	23	44	2.5	331	5	BU064153	BU064153 Fgr_4_E22
	24	44	2.5	389	5	BU065797	BU065797 Fgr_8_114

Matches 73; Conservative 139; Mismatches 167; Indels 0; Gaps 0;

972 TTTCCATAGAAATAAATCTAGTCTTTTATCTACCTGTAATGGTTTATTATTC 1031
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
629 TTTTAAATTTTWTWTAWATTTTITTTTAKTKTTTITTTTATTAATAAAAAAT 698
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1032 ATTAAGGGTAAAGTGGGGGCTTTAAATAAATCTCTGAATTTGATACATACATGTTA 1091
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
689 TDTWAAAWTTTTKKKKAAAAAADAADKADKADKADKADKADKADKADKADKADK 748
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1092 CACGGATATTGTTCTCTGGTCTGATATACATGTTTTCGAACGAGTCCGAGGCTACGT 1151
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
749 GKKGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 808
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1152 GGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTCTTTTGTGTTGGTT 1211
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
809 GKKGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 868
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1212 GGAAGTAATCAATAGTGAATCTAGGACAGTTTGGGGGTAAGTACCGGAGTGTAGG 1271
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
869 GGGKDDAAAKKKKGGTGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 928
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1272 AGAAGGGCTGGTGTATGTTGGGGGAGGAGTAGTTTACATAGGGGTACATAGTGGG 1331
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
929 GKKGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 988
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1332 CTGTGGCCTTTGTTACAAA 1350
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
989 KKKKKKKTKTKKKDAAA 1007
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 2
CNS00LOO/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BAC32223 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL068607
AL068607.1 GI:4958699
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Oosawa and
Aaron Mammeter in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
F1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1 . 1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR3223"
/clone_lib="RPCI-98"

/note="end : TET3"

ORIGIN
Query Match 2.7%; Score 47.8; DB 9; Length 1101;
Best Local Similarity 19.4%; Pred. No. 0.051; Indels 0; Gaps 0;
Matches 69; Conservative 135; Mismatches 151; Indels 0; Gaps 0;

999 TTTTATCACATTCGTAATGGTTTATTTATTTATTTATTTATTTATTTATTTATTTAA 1058
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1098 TTTTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1039
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1059 AATTAATTTCTCTGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1118
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1038 KTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 979
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1119 TACTGTTTTCGAACGAGTCCGAGGCTACATTTTCCAGCAGTTTGTAGTCT 1178
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
978 AAAAAADKKTDKARAKKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 919
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1179 TCAGGCACAGCTGGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1238
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
918 DTDWKKAGGGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 859
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1239 CAGGTTTGGGGTAAAGTACCGGAGTGTAGGAGAGGCTGGTATGTTATGTCGGGG 1298
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
858 AADGDAAAKTKTKKATWKKKGGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 799
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
1299 AGGAGTAGTTTACATAGGCTCATAGTGTAGGCTGTGGCTTTGTTTACAAAGTT 1353
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
798 TGDKKRTFWKTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 744
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 3
CA297536
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

661 bp mRNA linear EST 26-SEP-2003
SCCSD1C01F09.9 SD1 Saccharum officinarum cDNA clone SCCSD1C01F09
5', mRNA sequence.
CA297536
CA297536.1 GI:36066207
EST.
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 661)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bccc.net.br>
Plate: C01 row: F column: 09
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1 . 661
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCSD1C01F09"
/lab_host="DH10B"
/clone_lib="SD1"

/note="Organ: Developing seeds (large insert library);
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [Developing

vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.6%; Score 45.6; DB 6; Length 598;
Best Local Similarity 54.5%; Pred. No. 0.19;
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTCCAGCGGTAAACGGTGGCGGG 1641
Db 489 GCGGTAAACNCGCGCGCGCGTGGAGCGGTGGCGGCTACGCCGCCGTGATGAGGTGGCT 430
QY 1642 GTGACGACGAGCGCGCGCGCGGAGGATCTGGCAAGATGCTCGCGGGCGGTGTCT 1701
Db 429 ACGCGCGTGGCGCGCGCGCTACGCGCGGTGGCTACGGTGGCGGTGGTGGCT 370
QY 1702 TCTTCTTCGTTAAACGCTCTTGGATACGTCATATCTGAAAACGA 1746
Db 369 ACGCGCGGTGGCGCGCGCTACGGCACTCCGAGGGAACCTGA 325

RESULT 7
CA108913/c
LOCUS
DEFINITION
3', mRNA sequence.
ACCESSION
CA108913
VERSION
CA108913.1
KEYWORDS
EST.
SOURCE
Saccharum officinarum
ORGANISM
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE
1 (bases 1 to 667)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
CONTACT: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
Plate: 067 row: F column: 11
Seq primer: SP6 promoter primer.
Location/Qualifiers
1..667
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSGHR1067F11"
/lab_host="DH10B"
/clone_lib="HRI"
/note="Organ: seedlings inoculated with Herbaspirillum rubrisubalbicans; Vector: pSport1; Site:1: SalI; Site_2: NotI; An unidirectional cDNA library generated from seedlings inoculated with Herbaspirillum rubrisubalbicans). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

FEATURES
source

ORIGIN

leaves from in vitro grown seedlings). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.6%; Score 45.6; DB 6; Length 497;
Best Local Similarity 54.5%; Pred. No. 0.17;
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTCCAGCGGTAAACGGTGGCGGG 1641
Db 263 GCGGTAAACNCGCGCGCGCGTGGAGCGGTGGCGGCTACGCCGCCGTGATGAGGTGGCT 322
QY 1642 GTGACGACGAGCGCGCGCGCGGAGGATCTGGCAAGATGCTCGCGGGCGGTGTCT 1701
Db 323 ACGCGCGTGGCGCGCGCGCTACGCGCGGTGGCTACGGTGGCGGTGGTGGCT 382
QY 1702 TCTTCTTCGTTAAACGCTCTTGGATACGTCATATCTGAAAACGA 1746
Db 383 ACGCGCGGTGGCGCGCGCTACGGCACTCCGAGGGAACCTGA 427

RESULT 6
CA294459/c
LOCUS
DEFINITION
3', mRNA sequence.
ACCESSION
CA294459
VERSION
CA294459.1
KEYWORDS
EST.
SOURCE
Saccharum officinarum
ORGANISM
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE
1 (bases 1 to 598)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
CONTACT: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
Plate: 012 row: B column: 06
Seq primer: SP6 Promoter primer.
Location/Qualifiers
1..598
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSGHV1012B06"
/lab_host="DH10B"
/clone_lib="LV1"
/note="Organ: Etiolated leaves from in vitro grown seedlings; Vector: pSport1; Site:1: SalI; Site:2: NotI; An unidirectional cDNA library generated from [Etiolated leaves from in vitro grown seedlings]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the

FEATURES
source

Query Match 2.6%; Score 45.6; DB 6; Length 667;
 Best Local Similarity 54.5%; Pred. No. 0.19;
 Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAACATGCCATTTTCTCTCCAGCGGTAAAGTGGCGGG 1641
 |||||
 Db 459 GCGGNTACGGCGCGCGCGTGGAGCGGTGGCGGTACGGCGCGGTGATGAGGTGGCT 400
 |||||

QY 1642 GTGGACGACGCGGCGCGCGGAGGATCTGGCAAGATCGCTGCGGGCGCGGTCT 1701
 |||||
 Db 399 ACGGCGGTGGCGCGCGGTACGGCGGTGGCTACGGTGGCGGTGGCGGTGGCT 340
 |||||

QY 1702 TCTTCTCGGTACGCGCTCTTGGATAGCTATCTGAAACGA 1746
 |||||
 Db 339 ACGGCGGTGGCGCGGTACGGCAACTCGAGGGGAACCTGGA 295
 |||||

RESULT 8
 AI514058 561 bp mRNA linear EST 19-APR-2001
 LOCUS GH27112.5prime GH Drosophila melanogaster head pOT2 Drosophila
 DEFINITION melanogaster cDNA clone GH27112 5prime, mRNA sequence.
 ACCESSION AI514058
 VERSION AI514058.1 GI:4418120
 KEYWORDS EST.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 561)
 AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G.M.
 TITLE BDGP/HMMI Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd. Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: 271 row: A column: 12
 High quality sequence stop: 488.

FEATURES

source
 1..561
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="GH27112"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DHS - alpha"
 /clone_lib="GH Drosophila melanogaster head pOT2"
 /notes="Organ: head; Vector: pOT2; Site: 1: EcoRI; Site 2:
 XhoI; Sized fractionated cDNAs were directly ligated into
 pOT2. Plasmid cDNA library."

ORIGIN

Query Match 2.6%; Score 45.4; DB 1; Length 561;
 Best Local Similarity 58.5%; Pred. No. 0.21;
 Matches 79; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1569 TATATCGAAGTGGCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGGT 1628
 |||||
 Db 426 TATTCCGAGAGGTGGCGGAATCGCGGTGGAGGTGGCCATTCTGGTGAGGTAGCGGA 485
 |||||

QY 1629 AACGGTGGCGGGTGGACGAGCAGCGCGCGGAGCATCTGCCAAGATGGCTGC 1688
 |||||
 Db 486 ATCGTGGCGGCGCTGATTTGGTGGCGGAATCGGCGGAGGTGGCCATTCTGGTGA 545
 |||||

QY 1689 GGGGGCGGTCTCTTC 1703
 |||||
 Db 546 GCGGTGGATCTGC 560
 |||||

RESULT 9

CE373054/c 324 bp DNA linear GSS 27-SEP-2003
 LOCUS tigr-988-dog-17000362184725 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE373054
 VERSION CE373054.1 GI:36596968
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 324)
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers
 1..324
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 2.6%; Score 45.2; DB 9; Length 324;
 Best Local Similarity 54.9%; Pred. No. 0.2;
 Matches 89; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 963 TCGCCCTGAATTTCCATATGAAATAATTACTGAGTCTTTTTTATCACCTTCGTAATGGTTT 1022
 |||||
 Db 317 TGACTTTTAATCCCTTATAGATTCAGATATGAGTCTTCTTATCAACATGATAGTAT 258
 |||||

QY 1023 TTATTATTCAATTAAGGGTTAAGTGGGGGTCTTTAAATAAATTTCTCTGAATTGTACAT 1082
 |||||
 Db 257 ATATCATATGTATAGATCTATATGTATTAAAGATTAAAGATCTACATCTTAAATATCTATAT 198
 |||||

QY 1083 ACATGTTACACGGATTTGTTATTCCTGTCGTATATACCTGT 1124
 |||||
 Db 197 CTATAGATATACCTATCATATATATCTGTAGTATATCATAT 156
 |||||

RESULT 10

AG034053 1029 bp DNA linear GSS 01-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-009E13.F, genomic survey sequence.
 DEFINITION
 ACCESSION AG034053
 VERSION AG034053.1 GI:16560926
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE 1
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE BAC end sequences of Library PTB

Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott V. Tingey@USA.dupont.com
Seq primer: M13.

FEATURES
source
1. .571
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wialc.pk003.e22"
/tissue_type="anthers"
/lab_host="DH10B"
/clone_lib="wialc"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum, Hi Line) immature anthers"

ORIGIN
Query Match 2.5%; Score 45; DB 6; Length 571;
Best Local Similarity 57.4%; Pred. No. 0.27;
Matches 78; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1576 GAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGTAACGGTG 1635
Db 250 GGAGCGGTGCGAGTGGAGGAGCGGTGGAGCGGTCTGGAGGAGCGGCAGCAGCGGAG 309
QY 1636 GCGGGGGTGGACGAGCGAGCGCGCGCGGAGGATCTGGCAAGATGCTGGGGGGCG 1695
Db 310 GCGGATCTGGAGGAGCGCGCGCGGAGCGGATCANNAGGAGGTGGCAGCGCGCG 369
QY 1696 GTGTCTTCTTCTCGG 1711
Db 370 GCGGGTCCGCGGTGG 385

RESULT 12
CA103262 603 bp mRNA linear EST 23-SBP-2003
LOCUS SCEZHR1048D02.9 HR1 Saccharum officinarum cDNA clone SCEZHR1048D02
DEFINITION 5', mRNA sequence.
ACCESSION CA103262.1 GI:34956569
VERSION CA103262
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
REFERENCE 1 (bases 1 to 603)
AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
TITLE The libraries that made SUCESR
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 048 row: D column: 02
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .603
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEZHR1048D02"
/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirillum"

FEATURES
source
1. .603
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEZHR1048D02"
/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirillum"

Unpublished
2 (bases 1 to 1029)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, 305-8565, Japan
(E-mail: chimbies@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. .1029
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-009E13.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 2.6%; Score 45.2; DB 9; Length 1029;
Best Local Similarity 49.6%; Pred. No. 0.29;
Matches 116; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 978 TATGAATAAATACGAGTCTTTTATCACTTCGTAATGTTTATTTATTTATTTATTAAG 1037
Db 425 TATTTATGTTTATTTATTTATTTTCTCTGTTATTTTCTTTGTTTATTTATTTATTT 484
QY 1038 GGTAAAGTGGGGCTTTAAATTAATCTCTGATTTGATACATACATGTTTACACGA 1097
Db 485 ACTCAATATATGTTTGTCTTTTCTTTTCTATCTGTTTATTTATTTATTTATTTCA 544
QY 1098 TATTTATTCCTGCTGATATCTGTTTTCGAACGAGTGGCGCTACGTGTTCTA 1157
Db 545 TATTTTCTTTTCTTTTATTTATTTATTTATTTTCTTTCTTTTCTTTTCTTTTCTT 604
QY 1158 CATTTCCAGGTTTCTAGTCTCAGCAGCAGTGGTTCTTTGTTGTTTGT 1211
Db 605 CTTTCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 658

RESULT 11
CA741621 571 bp mRNA linear EST 26-NOV-2002
LOCUS wialc.pk003.e22 wialc Triticum aestivum cDNA clone wialc.pk003.e22
DEFINITION 5' end, mRNA sequence.
ACCESSION CA741621.1 GI:25557444
VERSION CA741621
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE 1 (bases 1 to 571)
AUTHORS Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
TITLE Dupont Wheat cDNA Sequence
JOURNAL Unpublished (2002)
COMMENT Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

rubrisubalbicans; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with *Herbaspirillum rubrisubalbicans*]. cDNA was prepared from polyA⁺ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.5%; Score 45; DB 6; Length 603;
Best Local Similarity 54.5%; Pred. No. 0.28;
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCACGCGGTACGCGGGG 1641

DB 97 GCGGCTACGCGCGCGCGGTGGAGCGGTGGCGGCTACGCGCGCGGTGATGGAGTGGCT 156

QY 1642 GTGGAGACCCAGGCGCGCGGAGGATCTGGCCAGCATGGCTGCGGGCGCGGTGCT 1701

DB 157 ACGCGGTGGCGCGCGCGGTACGCGCGGTGGCTACGCTGCGCGGTGGCGGTGGCT 216

QY 1702 TCTTCTTCGTAACGCTCTTGGATACGTATCTGAAACGA 1746

DB 217 ACGGCGCGGTGGCGCGGTACGCGCACTCCGAGGGGAACCTGGA 261

RESULT 13

CA300454

LOCUS SCSFLV1044D03.g 622 bp mRNA linear EST 26-SBP-2003

DEFINITION 5', mRNA sequence.

ACCESSION CA300454

VERSION CA300454.1 GI:36074598

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

1 (bases 1 to 622)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: 044 row: D column: 03

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1. .622

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCSFLV1044D03"

/lab_host="DH10B"

/clone_lib="LV1"

/note="Organ: Etiolated leaves from in vitro grown

seedlings; Vector: pSport1; Site_1: SalI; Site_2: NotI; An

unidirectional cDNA library generated from [Etiolated

leaves from in vitro grown seedlings]. cDNA was prepared

from polyA⁺ mRNA using SuperScript Plasmid System Kit

(Invitrogen). The double-strand cDNAs were fractionated

in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.5%; Score 45; DB 6; Length 622;
Best Local Similarity 54.5%; Pred. No. 0.28;
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCACGCGGTACGCGGGG 1641

DB 288 GCGGCTACGCGCGCGCGGTGGAGCGGTGGCGGCTACGCGCGCGGTGATGGAGTGGCT 347

QY 1642 GTGGAGACGACGAGCGCGCGGAGGATCTGGCCAAAGATGGCTGCGGGCGCGGTGCT 1701

DB 348 ACGGCGGTGGCGCGCGGCTACGCGCGGTGGCTACGCTGCGCGGTGGCTGCT 407

QY 1702 TCTTCTTCGTAACGCTCTTGGATACGTATCTGAAACGA 1746

DB 408 ACGGCGCGGTGGCGCGGTACGCGCACTCCGAGGGGAACCTGGA 452

RESULT 14

CA198894

LOCUS SCSFLV1079E04.g 640 bp mRNA linear EST 25-SBP-2003

DEFINITION 5', mRNA sequence.

ACCESSION CA198894

VERSION CA198894.1 GI:35230613

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

1 (bases 1 to 640)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: 079 row: E column: 04

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1. .640

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCSFLV1079E04"

/lab_host="DH10B"

/clone_lib="FL1"

/note="Organ: Inflorescence at beginning of development

(1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;

An unidirectional cDNA library generated from

[Inflorescence at beginning of development (1cm-long)]

cDNA was prepared from polyA⁺ mRNA using SuperScript

Plasmid System Kit (Invitrogen). The double-strand cDNAs

were fractionated in a sepharose CL-2B 40cm-columns and

fragments sizing between 0.8 and 1.5 Kb were

directionally cloned into the vector. Details of each

source of RNA and library construction can be obtained at

<http://sucet.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.5%; Score 45; DB 6; Length 640;
 Best Local Similarity 57.4%; Pred. No. 0.28;
 Matches 81; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1582 GCGGAGAGGGGGTGTGAAGATGCCATTTTCTCTCCAGCGGTAAACGTTGGCGGG 1641
 DB 369 GGGGCTACGGCGCGCGCGTGGAGCGGTGGCGGCTACGGCGCGCGTGTGAGGTGGCT 428

QY 1642 GTGGACGACCCAGGGCGGCGCGGAGGATCTGGGCAAGATGGCTCGGGGGCGGTGTCT 1701
 DB 429 ACGGCGGTGGCGCGCGGCTACGGCGCGGTGGCTACGGTGGCGGTGGCGGTGGCT 488

QY 1702 TCTTCTTCGGTAACGCTCTCTTGGATACGTATCTGAAACGA 1746
 DB 489 ACGGCGCGGTGGCGCGGCTACGGCAACTCGAGGGGAACCTGGA 533

Search completed: December 7, 2004, 21:41:23
 Job time : 5733 secs

RESULT 15

CA104948
 LOCUS SCJFHRIC03A05.9 HRI Saccharum officinarum cDNA clone SCJFHRIC03A05
 DEFINITION 721 bp mRNA linear EST 23-SEP-2003
 5' mRNA sequence.
 ACCESSION CA104948
 VERSION CA104948.1 GI:34958255
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE

1 (bases 1 to 721)
 Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
 The libraries that made SUCEST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: C03 row: A column: 05
 Seq primer: T7 Promoter Primer.

FEATURES

source
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 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCJFHRIC03A05"
 /lab_host="DH10B"
 /clone_lib="HRI"
 /note="Organ: seedlings inoculated with Herbaspirillum
 rubrisubalbicans; Vector: pSport1; Site_1: SalI; Site_2:
 NotI; An unidirectional cDNA library generated from
 (seedlings inoculated with Herbaspirillum
 rubrisubalbicans). cDNA was prepared from polyA+ mRNA
 using Superscript Plasmid System Kit (Invitrogen). The
 double-strand cDNAs were fractionated in a sepharose
 CL-2B 40cm-columns and fragments sizing between 0.8 and
 1.5 Kb were directionally cloned into the vector. Details
 of each source of RNA and library construction can be
 obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 2.5%; Score 45; DB 6; Length 721;
 Best Local Similarity 54.5%; Pred. No. 0.29;
 Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:39:01 ; Search time 7541 Seconds
(without alignments)
11080.878 Million cell updates/sec

Title: US-10-718-264-15
Perfect score: 1767
Sequence: 1 accagcgacttcggcagcg.....agaagtgcgtgtaagtatt 1767

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1767	100.0	1767	6	AR482255	Sequence
2	1767	100.0	1767	6	AR482256	Sequence
3	1767	100.0	1767	6	AX003274	Sequence
4	1767	100.0	1767	6	AX003275	Sequence
5	1757.4	99.5	1767	14	AY321984	Porcine c
6	1755.8	99.4	1767	14	AF201897	Porcine c
7	1755.8	99.4	1767	14	AY321985	Porcine c
8	1755.8	99.4	1767	14	AY321986	Porcine c
9	1752.6	99.2	1767	14	AY256460	Porcine c
10	1752.6	99.2	1767	14	AY321989	Porcine c
11	1752.6	99.2	1767	14	AY322000	Porcine c
12	1751	99.1	1767	14	AY188355	Porcine c
13	1751	99.1	1767	14	AY217743	Porcine c
14	1751	99.1	1767	14	AY321988	Porcine c
15	1751	99.1	1767	14	AY321990	Porcine c
16	1751	99.1	1767	14	AY321992	Porcine c
17	1751	99.1	1767	14	AY321994	Porcine c
18	1751	99.1	1767	14	AY321997	Porcine c
19	1751	99.1	1767	14	AY322001	Porcine c

20	1751	99.1	1767	14	AY322002	Porcine c
21	1751	99.1	1767	14	AY244405	Porcine c
22	1751	99.1	1767	14	AY536755	Porcine c
23	1751	99.1	1767	14	AY604430	Porcine c
24	1751	99.1	1767	14	AY613854	Porcine c
25	1749.4	99.0	1767	14	AY321987	Porcine c
26	1749.4	99.0	1767	14	AY321995	Porcine c
27	1749.4	99.0	1767	14	AY321998	Porcine c
28	1749.4	99.0	1767	14	AY321999	Porcine c
29	1747.8	98.9	1767	14	AY181945	Porcine c
30	1747.8	98.9	1767	14	AY321991	Porcine c
31	1747.8	98.9	1767	14	AY321996	Porcine c
32	1747.8	98.9	1767	14	AY244404	Porcine c
33	1746.2	98.8	1767	14	AY177626	Porcine c
34	1746.2	98.8	1767	14	AY256457	Porcine c
35	1746.2	98.8	1767	14	AY291316	Porcine c
36	1746.2	98.8	1767	14	AY536756	Porcine c
37	1746.2	98.8	1767	14	AY641542	Porcine c
38	1746.2	98.8	1767	14	AY651850	Porcine c
39	1741.4	98.6	1767	14	AY317129	Porcine c
40	1739.8	98.5	1767	14	AY596823	Porcine c
41	1736.6	98.3	1767	14	AY321982	Porcine c
42	1736.6	98.3	1767	14	AY321983	Porcine c
43	1735.6	98.2	1766	14	PCI293869	Porcine c
44	1735	98.2	1767	14	AY322003	Porcine c
45	1733	98.1	1778	14	AY321993	Porcine c

ALIGNMENTS

RESULT 1
AR482255
LOCUS AR482255 1767 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 15 from patent US 6703023.
ACCESSION AR482255
VERSION AR482255.1 GI:47244296
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1767)
AUTHORS Jestin,A., Albina,E., Le Cann,P., Blanchard,P., Hutet,E.,
Arnault,C., Truong,C., Mahe,D., Cariolet,R. and Madec,F.
TITLE Citrovirus sequences associated with piglet weight loss disease
(PMD)
JOURNAL Patent: US 6703023-A 15 09-MAR-2004;
FEATURES Location/Qualifiers
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/organism="unknown"
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DB	121	CTTCCGAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA	180		
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ACCESSION AR482256
VERSION AR482256.1 GI:47244297
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1767)
AUTHORS Jestin,A., Albina,E., Le Cann,P., Blanchard,P., Hutet,E.,
Arnould,C., Truong,C., Mahe,D., Cariolet,R. and Madec,P.
Circovirus sequences associated with piglet weight loss disease
(PWD)
JOURNAL Patent: US 6703023-A 19 09-MAR-2004;
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred.No.0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 10 from Patent WO9929871.
ACCESSION AX003275
VERSION    AX003275.1  GI:9927099
KEYWORDS   Porcine circovirus
SOURCE     Porcine circovirus
ORGANISM   Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE  1
AUTHORS    Hutet, E., Albina, E., Arnaud, C., Cariolet, R., Jestin, A., Le, C.P.,
Maded, F., Mahe, D., Blanchard, P. and Truong, C.
TITLE      Circovirus sequences related to piglet weight loss disease (pwd)
JOURNAL    Patent: WO 9929871-A 10 17-JUN-1999;
HUTET EVELYNE (FR); ALBINA EMMANUEL (FR); ARNAUD CLAIRE (FR);
CARIOLET ROLAND (FR); JESTIN ANDRE (FR); LE CANN PIERRE (FR); MADEC
FRANCOIS (FR); MAHE DOMINIQUE (FR); BLANCHARD PHILIPPE (FR); TRUONG
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 SOURCE Porcine circovirus 2
 ORGANISM Porcine circovirus 2
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 AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
 Eveno, E., Mader, F. and Jestin, A.
 TITLE Molecular characterization of Porcine circovirus type 2 isolates
 from post-weaning multisystemic wasting syndrome-affected and
 non-affected pigs
 J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
 JOURNAL 14769887
 PUBMED 2 (bases 1 to 1767)
 REFERENCE de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
 Eveno, E., Mader, F. and Jestin, A.
 AUTHORS Direct Submission
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 Food Safety Agency, Bp 53, Ploufragan 22 440, France
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Query Match 99.5%; Score 1757.4; DB 14; Length 1767;
Best Local Similarity 99.7%; Pred. No. 0;
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ACCESSION AV321985
VERSION AV321985.1 GI:32478763


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KEYWORDS Porcine circovirus 2
SOURCE Porcine circovirus 2
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1767)
AUTHORS de Boisseson,C., Beven,V., Bigarre,L., Thierry,R., Rose,N.,
Eveno,E., Mader,P. and Jestin,A.
TITLE Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
14769887
REFERENCE 2 (bases 1 to 1767)
AUTHORS de Boisseson,C., Beven,V., Bigarre,L., Thierry,R., Rose,N.,
Eveno,E., Mader,P. and Jestin,A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
Food Safety Agency, BP 53, Ploufragan 22 440, France
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1 (bases 1 to 1767)
Dan,A., Molnar,T., Biksei,I., Glavits,R., Shaheim,M.A. and
Harrach,B.
Characterisation of Hungarian porcine circovirus 2 genomes
associated with PMNS and PDNS cases
Acta Vet. Hung. 51 (4), 551-562 (2003)
2 (bases 1 to 1767)
Harrach,B.
Direct Submission
Submitted (14-MAR-2003) Veterinary Medical Research Institute,
Hungarian Academy of Sciences, Hungary krt. 21, Budapest H-1143,
Hungary
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Db 1741 AAACGAAAGAGTGGCTGTAAGTATT 1767
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LOCUS
DEFINITION Porcine circovirus type 2 strain 375 replicase (rep) and putative
capsid protein (cap) genes, complete cds.
ACCESSION AY256460
VERSION AY256460.1 GI:37595458
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
Viruses; ssDNA viruses; Circoviridae; Circovirus.

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DEFINITION Porcine circovirus 2 strain Fd12, complete genome.
ACCESSION AY321989
VERSION AY321989.1 GI:32478775
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
REFERENCE 1 (bases 1 to 1767)
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
TITLE Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
JOURNAL J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
PUBMED 14763887
REFERENCE 2 (bases 1 to 1767)
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
Food Safety Agency, BP 53, Ploufragan 22 440, France
FEATURES
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LOCUS Porcine circovirus type 2 strain HZ0201, complete genome.
DEFINITION Porcine circovirus type 2 strain HZ0201, complete genome.
ACCESSION AY188355
VERSION AY188355.1 GI:28396146
KEYWORDS Porcine circovirus 2
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1767)
Zhou,J.Y., Chen,Q.X., Ye,J.X., Chen,W.J., Chen,J.G., Cheng,L.Q. and
Shang,S.B.
Complete genome of HZ0201 strain of PCV-2 isolated from sows with
various clinical syndromes
Unpublished
JOURNAL 2 (bases 1 to 1767)
Zhou,J.Y., Chen,Q.X., Ye,J.X., Chen,W.J., Chen,J.G., Cheng,L.Q. and
Shang,S.B.
Direct Submission
JOURNAL Submitted (26-NOV-2002) Institute of Preventive Veterinary
Medicine, Zhejiang University, 268 Kaixuan Road, Hangzhou, Zhejiang
310029, P.R.China
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DEFINITION Porcine circovirus type 2 strain HZ0202, complete genome.
ACCESSION AY217743
VERSION AY217743.1 GI:28932891
KEYWORDS Porcine circovirus 2
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ORGANISM

Porcine circovirus 2
Viruses; ssDNA viruses; Circoviridae; Circovirus.

REFERENCE

1. (bases 1 to 1767)
Zhou, J.Y., Chen, Q.X., Ye, J.X., Wang, J.Y., Chen, J.G., Chen, W.J. and Zheng, X.J.

TITLE

Complete genome of PCV-2 strain HZ0202 isolated from sows with various clinical syndrome

JOURNAL

Unpublished

REFERENCE

2. (bases 1 to 1767)
Zhou, J.Y., Chen, Q.X., Ye, J.X., Wang, J.Y., Chen, J.G., Chen, W.J. and Zheng, X.J.

TITLE

Direct Submission
Submitted (13-JAN-2003) Zhejiang University, Institute of Preventive Veterinary Medicine, 268 Kaixuan Road, Hangzhou, Zhejiang 310029, P.R. China

FEATURES

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ORIGIN

Query Match 99.1%; Score 1751; DB 14; Length 1767;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1757; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 14
AY321988
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DEFINITION Porcine circovirus 2
ACCESSION AY321988
VERSION AY321988.1 GI:32478772
KEYWORDS Porcine circovirus 2
SOURCE Porcine circovirus 2
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1767)
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
TITLE Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
PUBMED 14769887
REFERENCE 2 (bases 1 to 1767)
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
Food Safety Agency, BP 53, Ploufragan 22 440, France
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CDS

ORIGIN

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RESULT 15

AV321990

LOCUS

DEFINITION

1767 bp DNA circular VRL 11-FEB-2004
Porcine circovirus 2 strain Fd7, complete genome.

Wed Dec 8 12:30:20 2004

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KEYWORDS		Db	301	AGAAAGCGAAAGGAACAGATCAGCAGAAATAAAGAAATACTGCAGTAAGAAAGGCAACTTAC	360
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ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.	Db	361	TGATGGAGTGGAGCTCCTAGATCTCAGGACAAACGGAGTGACCTGTCTACTGCTGGA	420
REFERENCE	1 (bases 1 to 1767)	Qy	421	GTACCTTTGTCGAGAGCGGAGTCTGGTGACCGTTTGACAGACAGCACCCTCTGAAGCTTTG	480
AUTHORS	de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Eveno,E., Madec,F. and Jestin,A.	Db	421	GTACCTTTGTCGAGAGCGGAGTCTGGTGACCGTTTGACAGACAGCACCCTCTGAAGCTTTG	480
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JOURNAL	J. Gen. Virol. 85 (Pt 2), 293-304 (2004)	Db	481	TCAGAAATTTCCGGCGGCTGGCTGAACATTTTGAAGTGAGCGGGAANAATCAGAAAGCGTG	540
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AUTHORS	de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Eveno,E., Madec,F. and Jestin,A.	Qy	601	CTGCTAATTTTTCAGACCCCGGAAACCACTACTGGAACCACTTAGAAGCAAGTGGTGGG	660
TITLE	Direct Submission	Db	601	CTGCTAATTTTTCAGACCCCGGAAACCACTACTGGAACCACTTAGAAGCAAGTGGTGGG	660
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Qy	121	CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA	180		
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GenCore version 5.1.6
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Run on: December 7, 2004, 17:40:24 ; Search time 158 Seconds
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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43	886.4	50.2	1759	4	US-09-583-350-5
44	886.4	50.2	1759	4	US-09-884-514-5
45	702	39.7	702	4	US-09-514-245-25

ALIGNMENTS

RESULT 1

US-09-514-245-15
; Sequence 15, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Type B PWD circovirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(111)
; NAME/KEY: CDS
; LOCATION: (115)..(243)
; NAME/KEY: CDS
; LOCATION: (247)..(267)
; NAME/KEY: CDS
; LOCATION: (271)..(360)
; NAME/KEY: CDS
; LOCATION: (364)..(417)
; NAME/KEY: CDS
; LOCATION: (421)..(447)
; NAME/KEY: CDS
; LOCATION: (451)..(471)
; NAME/KEY: CDS
; LOCATION: (475)..(510)
; NAME/KEY: CDS
; LOCATION: (514)..(516)
; NAME/KEY: CDS
; LOCATION: (520)..(729)
; NAME/KEY: CDS
; LOCATION: (733)..(753)

Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 163, App
Sequence 5, Appli
Sequence 38, Appl
Sequence 40, Appl
Sequence 164, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 13, Appl
Sequence 23, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 25, Appli

/	NAME/KEY:	CDS
/	LOCATION:	(757) .. (759)
/	NAME/KEY:	CDS
/	LOCATION:	(763) .. (804)
/	NAME/KEY:	CDS
/	LOCATION:	(808) .. (861)
/	NAME/KEY:	CDS
/	LOCATION:	(865) .. (984)
/	NAME/KEY:	CDS
/	LOCATION:	(988) .. (1173)
/	NAME/KEY:	CDS
/	LOCATION:	(1177) .. (1233)
/	NAME/KEY:	CDS
/	LOCATION:	(1237) .. (1359)
/	NAME/KEY:	CDS
/	LOCATION:	(1363) .. (1476)
/	NAME/KEY:	CDS
/	LOCATION:	(1480) .. (1737)
/	NAME/KEY:	CDS
/	LOCATION:	(1741) .. (1767)
/	US-09-514-245-15	
Query Match		
Best Local Similarity 100.0%; Score 1767; DB 4; Length 1767;		
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ACCAAGCCACTTCGGCAGCGGACGACCTCGGCAGCACCTCAGCAGCAAATGCCACGA 60
Dd	1	ACCAGCGCACTTCGGCAGCGGACGACCTCGGCAGCACCTCAGCAGCAAATGCCACGA 60
Qy	61	AGAAGAATTGGAAGAACGGGACCCCAACCCCATAAAGTGGGTGTTCATCTGAATTAATC 120
Dd	61	AGAAGATGGAAGAACGGGACCCCAACCCCATAAAGTGGGTGTTCATCTGAATTAATC 120
Qy	121	CTTCCGAAGACAGCGGCAAGAAATACGGGATCTCCAATATCCCTATTTCGATTTTAA 180
Dd	121	CTTCCGAAGACAGCGGCAAGAAATACGGGATCTCCAATATCCCTATTTCGATTTTAA 180
Qy	181	TGTTGGCGAGGAGGTAAATGAGGAAGGACGAACAACCTCACTCCAGGGTTCGCTAAT 240
Dd	181	TGTTGGCGAGGAGGTAAATGAGGAAGGACGAACAACCTCACTCCAGGGTTCGCTAAT 240
Qy	241	TGTGAAGACAGACTTTTTTAATAAGTGAAGTGTATTGGTGCCCGCTGCCACATCG 300
Dd	241	TGTGAAGACAGACTTTTTTAATAAGTGAAGTGTATTGGTGCCCGCTGCCACATCG 300
Qy	301	AGAAAGCAAGGAACAGATCAGCAGATAAAGAATACTGCAGTAAAGAAGCAACTTAC 360
Dd	301	AGAAAGCAAGGAACAGATCAGCAGATAAAGAATACTGCAGTAAAGAAGCAACTTAC 360
Qy	361	TGATGGAGTGTGGAGCTCTTAGATCTCAGGGAACAAGAGTGACCTGTCTACTGCTGA 420
Dd	361	TGATGGAGTGTGGAGCTCTTAGATCTCAGGGAACAAGAGTGACCTGTCTACTGCTGA 420
Qy	421	GTAACCTTGTGAGAGCGGGAGCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGTTTG 480
Dd	421	GTAACCTTGTGAGAGCGGGAGCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGTTTG 480
Qy	481	TCAGAAATTCGCGCGGCTGGCTGAACTTTTGAAGGTGACGGGAAAAATGCAGAGCGGTG 540
Dd	481	TCAGAAATTCGCGCGGCTGGCTGAACTTTTGAAGGTGACGGGAAAAATGCAGAGCGGTG 540
Qy	541	ATTGGAAGACTAATGTACAGCTCATTTGTGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
Dd	541	ATTGGAAGACTAATGTACAGCTCATTTGTGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
Qy	601	CTGCTAATTTTGAGACCCGGAAACACACATACTGGAAGAACCACTAGAAAACAAGTGGTGG 660
Dd	601	CTGCTAATTTTGAGACCCGGAAACACACATACTGGAAGAACCACTAGAAAACAAGTGGTGG 660
Qy	661	ATGGTTACATGGTGAAGAGTGGTTTATTTGATGACTTTTATGCTGGCTGCCTGGG 720
Dd	661	ATGGTTACATGGTGAAGAGTGGTTTATTTGATGACTTTTATGCTGGCTGCCTGGG 720

RESULT 2
US-09-514-245-19/c
; Sequence 19, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CAROLET, Roland
; APPLICANT: MADSC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Type B PWD circovirus
US-09-514-245-19

Query Match	100.0%	Score 1767;	DB 4;	Length 1767;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1767;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	ACCAGCGCACTTCGGCAGCGGAGCAGCACTCGGAGCACTCAGCAGCAACATGCCAGCA	60		
DB 1767	ACCAGCGCACTTCGGCAGCGGAGCAGCACTCGGAGCACTCAGCAGCAACATGCCAGCA	1708		
QY 61	AGAGNATCGAAGAGCGGACCCCAACCCCATAAAGTGGGTTCACCTCTGAATAATC	120		
DB 1707	AGAGNATCGAAGAGCGGACCCCAACCCCATAAAGTGGGTTCACCTCTGAATAATC	1648		
QY 121	CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTTTAA	180		
DB 1647	CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTTTAA	1588		
QY 181	TTGTTGGCAGGAGGGAATAGGAAGAGCAACCTCACCTCCAGGGGTCGCTAAT	240		
DB 1587	TTGTTGGCAGGAGGGAATAGGAAGAGCAACCTCACCTCCAGGGGTCGCTAAT	1528		
QY 241	TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGGTATTTGGTGCCCGTCGCACATCG	300		
DB 1527	TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGGTATTTGGTGCCCGTCGCACATCG	1468		
QY 301	AGAAAGCGAAAGCAAGATCAGCAGAAATAAGAACTGCGAGTAAAGAGGCAACTTAC	360		
DB 1467	AGAAAGCGAAAGCAAGATCAGCAGAAATAAGAACTGCGAGTAAAGAGGCAACTTAC	1408		
QY 361	TGATGGAGTGTGGAGCTCCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTGTGTGA	420		
DB 1407	TGATGGAGTGTGGAGCTCCTAGATCTCAGGAGCAACCGAGTGACCTGTCTACTGTGTGA	1348		
QY 421	GTACCTTTTGGAGAGCGGAGTCTGGTGACCGTTGAGAGAGCAGACCTGTAAACGTTTG	480		
DB 1347	GTACCTTTTGGAGAGCGGAGTCTGGTGACCGTTGAGAGAGCAGACCTGTAAACGTTTG	1288		
QY 481	TCAGAAATTTCCGGGCTGGCTGAACTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	540		
DB 1287	TCAGAAATTTCCGGGCTGGCTGAACTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	1228		
QY 541	ATTGGAAGACTAATGTACACGTCAATTTGTGGGGCCACCTGGGTTGGTAAAGCAATGGG	600		
DB 1227	ATTGGAAGACTAATGTACACGTCAATTTGTGGGGCCACCTGGGTTGGTAAAGCAATGGG	1168		

QY	601	CTGCTAAATTTTGCAGACCCCGGAAACCAATACCTAGAAACCACTAGAAACCAAGTGGTGGG	660
DB	1167	CTGCTAAATTTTGCAGACCCCGGAAACCAATACCTAGAAACCACTAGAAACCAAGTGGTGGG	1108
QY	661	ATGGTTACCATGGTGAAGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG	720
DB	1107	ATGGTTACCATGGTGAAGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG	1048
QY	721	ATGATCTACTCAGACTGTGATCGATATCATTTGACTGTAGAGACTAAAGTGGAACTG	780
DB	1047	ATGATCTACTCAGACTGTGATCGATATCATTTGACTGTAGAGACTAAAGTGGAACTG	988
QY	781	TACCTTTTTCGCCCGCAGATATCTGATTAACAGCAATCAGACCCCGTGGAACTGGTACT	840
DB	987	TACCTTTTTCGCCCGCAGATATCTGATTAACAGCAATCAGACCCCGTGGAACTGGTACT	928
QY	841	CCTCAACTGCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT	900
DB	927	CCTCAACTGCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT	868
QY	901	GGAGAAATGCTACAGAACCAATCCACGAGAGGAGGCGCAGTTCGTCAACCTTTCCGCC	960
DB	867	GGAGAAATGCTACAGAACCAATCCACGAGAGGAGGCGCAGTTCGTCAACCTTTCCGCC	808
QY	961	CATGCCCTGAAATTTCCATATGAAATTAATTAAGTCTTTTATCACTTCGTAAATGGT	1020
DB	807	CATGCCCTGAAATTTCCATATGAAATTAATTAAGTCTTTTATCACTTCGTAAATGGT	748
QY	1021	TTTTATTAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTAATTAATTAATTAATTAAT	1080
DB	747	TTTTATTAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTAATTAATTAATTAATTAAT	688
QY	1081	ATACATGTTTACACGGATATTTGATTTCTGGTGGTATATCTGTCTTTCGAAAGCGAGTGC	1140
DB	687	ATACATGTTTACACGGATATTTGATTTCTGGTGGTATATCTGTCTTTCGAAAGCGAGTGC	628
QY	1141	GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT	1200
DB	627	GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT	568
QY	1201	GTGTTTGGTGGAAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG	1260
DB	567	GTGTTTGGTGGAAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG	508
QY	1261	GGAGTGTAGGAGAGGCTGGTTATGATGCGGAGGAGTGTAGTTCATAGGGGTC	1320
DB	507	GGAGTGTAGGAGAGGCTGGTTATGATGCGGAGGAGTGTAGTTCATAGGGGTC	448
QY	1321	ATAGGTGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCAGTGGAGCC	1380
DB	447	ATAGGTGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCAGTGGAGCC	388
QY	1381	CACTCCCTGTCCCTGGTGTATCGGGAGCAGGCGCCAGAAATTCACCTTAACCTTTCT	1440
DB	387	CACTCCCTGTCCCTGGTGTATCGGGAGCAGGCGCCAGAAATTCACCTTAACCTTTCT	328
QY	1441	TATCTGTAGTATCAAGGGCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAAGAAA	1500
DB	327	TATCTGTAGTATCAAGGGCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAAGAAA	268
QY	1501	GTCAATTAATTTGAATCTCATGTCCACCGCCAGGAGGGGCTTCTGACTGTGGTTCG	1560
DB	267	GTCAATTAATTTGAATCTCATGTCCACCGCCAGGAGGGGCTTCTGACTGTGGTTCG	208
QY	1561	CTTGAAGTATATCCGAAGTGGGAGAGGGGGTGTGGAAGATGCCATTTTCTCTCT	1620
DB	207	CTTGAAGTATATCCGAAGTGGGAGAGGGGGTGTGGAAGATGCCATTTTCTCTCT	148
QY	1621	CCAGCGGTAAACGGTGGCGGGGTGGACGAGCCAGGGGCGCGCGGAGGATCTGGGCAAG	1680
DB	147	CCAGCGGTAAACGGTGGCGGGGTGGACGAGCCAGGGGCGCGCGGAGGATCTGGGCAAG	88

Qy 1681 ATGCTGCGGGGGGGTGTCTTCTTTCGGTAACGCTCTTGGATACGTATATCTGA 1740
Db 87 ATGCTGCGGGGGGGTGTCTTCTTTCGGTAACGCTCTTGGATACGTATATCTGA 28
Qy 1741 AAACGAAGAAGTGGCTGTAAAGTATT 1767
Db 27 AAACGAAGAAGTGGCTGTAAAGTATT 1
RESULT 3
US-09-583-350-8
; Sequence 8, Application US/09583350
; Patent No. 6517843
; GENERAL INFORMATION:
; APPLICANT: Ellis, et al.
; TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION AS
; TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2
; FILE REFERENCE: 454313-2340-1
; CURRENT APPLICATION NUMBER: US/09/583,350
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/151,564
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-583-350-8
Query Match 92.9%; Score 1642.4; DB 4; Length 1768;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
Qy 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60
Db 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60
Qy 61 AGAAGAATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTCTCACTCTGTAATATC 120
Db 61 AGAAGAATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTCTCACTCTGTAATATC 120
Qy 121 CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTGA 180
Db 121 CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTGA 180
Qy 181 TTGTTGGCGAGGAGGTATAGGAAGGACGAACTCACTCACTCACTCACTCACTCACT 240
Db 181 TTGTTGGCGAGGAGGTATAGGAAGGAGCAACCTCACCTCCAGGGGTTTCGCTAAT 240
Qy 241 TTGTGAAGAGCAGACTTTTATTAAGTGAAGTGTATTTGGTGGCGGCTGCCACATCG 300
Db 241 TTGTGAAGAGCAGAACTTTTATTAAGTGAAGTGTATTTGGTGGCGGCTGCCACATCG 300
Qy 301 AGAAGCGAAGGAAACAGATCAGCAGATAAAGATCTGCACTAAAGAGCAACTTAC 360
Db 301 AGAAGCGAAGGAACTGATCAGCAGATAAAGATCTGCACTAAAGAGCAACTTAC 360
Qy 361 TGA TGAAGTGTGAAGTCTTGAATCTCAGGGAACAGGAGTGCCTGTCTACTGTGTA 420
Db 361 TTATTGAATGTGAAGTCTTGAATCTCAGGGAACAGGAGTGCCTGTCTACTGTGTA 420
Qy 421 GTACCTTGTGGAGAGCGGGAGTCTGGTACCGTTCAGAGCAGCAGCCTGTAAACGTTG 480
Db 421 GTACCTTGTGGAGAGCGGGAGTCTGGTACCGTTCAGAGCAGCAGCCTGTAAACGTTG 480
Qy 481 TCAGAAATTTCCGGGGCTGGCTGAATTTTGAAGTGAAGCGGGAATAATCGAAGCGGTG 540
Db 481 TCAGAAATTTCCGGGGCTGGCTGAATTTTGAAGTGAAGCGGGAATAATCGAAGCGGTG 540
Qy 541 ATTGGAAGACTAATGTACAGTCTATTTGGGGGCCACCTGGTGTGTAAAGCAATGGG 600
Db 541 ATTGGAAGCAATGTACAGTCTATTTGGGGGCCACCTGGTGTGTAAAGCAATGGG 600

Qy 601 CTGCTAAATTTTGCAGACCCGGAACACATATCTGGAACCCACCTAGAAACAAAGTGGTGG 660
Db 601 CTGCTAAATTTTGCAGACCCGGAACACATATCTGGAACCCACCTAGAAACAAAGTGGTGG 660
Qy 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATGATGACTTTATGCTGGCTGGCTGGCTGG 720
Db 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATGATGACTTTATGCTGGCTGGCTGGCTGG 720
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCACCTGTAGAGACTAAAGTGGAACTG 780
Db 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCACCTGTAGAGACTAAAGTGGAACTG 780
Qy 781 TACCTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTTGGAAATGGTACT 840
Db 781 TACCTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTTGGAAATGGTACT 840
Qy 841 CTTCAACTCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCTTGGTATT 900
Db 841 CTTCAACTCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCTTGGTATT 900
Qy 901 GGAAGATGCTACAGAAACAAATCCAGGAGAAAGGGGCCAGTTCGTCACTTCCCTCCC 960
Db 901 GGAAGATGCTACAGAAACAAATCCAGGAGAAAGGGGCCAGTTCGTCACTTCCCTCCC 960
Qy 961 CATGCCCTGAAATTTCCATATGAAATTAATCTAGTCTTTTATCTACCTCTGTAATGGT 1020
Db 961 CATGCCCTGAAATTTCCATATGAAATTAATCTAGTCTTTTATCTACCTCTGTAATGGT 1020
Qy 1021 TTTTATATTTCA-TTAAAGGTTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAAATGTA 1079
Db 1021 TTTTATATTTCA-TTAAAGGTTTAAAGTGGGGGCTTTTAAAGTAAATTTCTCTGAAATGTA 1080
Qy 1080 CATACATGTTTACACGGATATGTAATCTCTGTGCTGATATCTACTGTTTTCGAACGAGTGC 1139
Db 1081 CATACATGTTTACACGGATATGTAATCTCTGTGCTGATATCTACTGTTTTCGAACGAGTGC 1140
Qy 1140 CGAGGCTACGCTGCTTACATTTTCCAGCAGTCTTGTAGTCTCAGCCACAGCTGCTTCTTT 1199
Db 1141 CGAGGCTACGCTGCTTACATTTTCCAGCAGTCTTGTAGTCTCAGCCCAAGAGCTGATCTCT 1200
Qy 1200 TGTGTTGTTGCTCGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTTAAAGTACC 1259
Db 1201 TGTGTTGTTGCTCGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTGTAGTAAC 1260
Qy 1260 GGAAGTGTAGGAGAGGCTGGGTTATGCTATGCGGAGGAGTGTATTTACATAGGGGT 1319
Db 1261 GGAAGTGTAGGAGAGGCTGGGTTATGCTATGCGGAGGAGTGTATTTACATATGGGT 1320
Qy 1320 CATAGGTGAGGCTGTGGCTTTGTTACAAAGTATCATCTAATAAATAACAGCACTGGAGC 1379
Db 1321 CATAGGTGAGGCTGTGGCTTTGTTACAAAGTATCATCTAATAAATAACAGCACTGGAGC 1380
Qy 1380 CCCTCCCTCTGACCTGGGTGATCGGGAGCAGGCGCAGAAATTTCAACCTTAACTTTTC 1439
Db 1381 CCCTCCCTCTGACCTGGGTGATCGGGAGCAGGCGCAGAAATTTCAACCTTAACTTTTC 1440
Qy 1440 TTATTCTGTAGTATTTCAAGGCGCACAGCGGGGGTTTGAACCCCTCTCTGGGGGAGAA 1499
Db 1441 TTATTCTGTAGTATTTCAAGGCGTATAGAGATTTTGTGGTCCCCCTCCCCGGGGGAAACA 1500
Qy 1500 AGTCAATTAATTTCAATCTCATCTGTCACCGCCAGGAGGGGCTTCTGACTGTGGTTC 1559
Db 1501 AGTCAATTAATTTCAATCTCATCTGTCACCGCCAGGAGGGGCTTCTGACTGTGGTTC 1560
Qy 1560 GCTTGACAGTATATCCGAAAGTGGGGAGAGCGGGGTGTTGAAGATGCCATTTTTCCTTC 1619
Db 1561 GCTTGACAGTATATCCGAAAGTGGGGAGAGCGGGGTGTTGAAGATGCCATTTTTCCTTC 1620
Qy 1620 TCCAGCGGTAAACGTTGCGGGGGTGGACAGCCAGGGGGCGGGGAGGATCTGGGCAA 1679
Db 1621 TCCAGCGGTAGCGGTGGGGGGTGGACAGCCAGGGGGCGGGGAGGATCTGGGCAA 1680

QY 1620 TCACGCGGTAAACGCTGGCGGGTGGACGACCGCAGCGCGCGCGCGAGGATCTGGCCAA 1679
DB 1621 TCACGCGGTAGCGTGGCGGGTGGACGACCGCAGCGCGCGCGCGAGGATCTGGCCAA 1680
QY 1680 GATGGCTGGCGGGCGGTGCTCTTCTTCTGGTAACCGCTCTTGGATAGCTCATATCTG 1739
DB 1681 GATGGCTGGCGGGCGGTGCTCTTCTTCTGGGTAAACCGCTCTTGGATATGTCAATCTG 1740
QY 1740 AAAACGAAAGAGTGGCTGTAAAGTATT 1767
DB 1741 AAAACGAAAGAGTGGCTGTAAAGTATT 1768
RESULT 5
US-10-112-540-1
; Sequence 1, Application US/10112540
; Patent No. 6794163
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; APPLICANT: Tikoo, Suresh K.
; APPLICANT: Willson, Philip
; APPLICANT: Babluk, Lorne A.
; TITLE OF INVENTION: METHODS TO CULTURE CIRCOVIRUS
; FILE REFERENCE: 293102003100
; CURRENT APPLICATION NUMBER: US/10/112,540
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/279,173
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-10-112-540-1
Query Match 91.7%; Score 1620; DB 4; Length 1768;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1682; Conservative 0; Mismatches 85; Indels 1; Gaps 1;
QY 1 ACCAGCGCACTTCGGCAGCGCGCAGCACTTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60
DB 1 ACCAGCGCACTTCGGCAGCGCGCAGCACCTTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60
QY 61 AGAAGAAATGGAAAGACGGACCCCAACCCCAATAAAGTGGGTCTACTCTGAATAATC 120
DB 61 AGAAGAAATGGAAAGACGGACCCCAACCAACATAAAGTGGGTCTCAGCTGAATAATC 120
QY 121 CTTCCGACAGCAGCGCAAGAAATACGGATCTTCCATATCCCTATTGATTAATTTA 180
DB 121 CTTCCGACAGCAGCGCAAGAAATACGGAGCTCCCAATCTCCCTATTGATTAATTTA 180
QY 181 TTGTTCCGAGAGGGTAAATAGGAAGACGAAACACCTCACCTCCAGGGGTTTCGTAATT 240
DB 181 TTGTTCCGAGAGGGTAAATAGGAAGACGAAACACCTCACCTCCAGGGGTTTCGTAATT 240
QY 241 TTGTGAAGACGACGACTTTTAATAAGTGAAGTGGTATTGGTGCCCGCTGCCACATCG 300
DB 241 TTGTGAAGACGACGACTTTTAATAAGTGAAGTGGTATTGGTGCCCGCTGCCACATCG 300
QY 301 AGAAGCGAAGGAAACAGATCAGCAGATAAAGAACTTGCAGTAAAGAGGCAACTTAC 360
DB 301 AGAAGCGAAGGAAACAGATCAGCAGATAAAGAACTTGTAGTAAAGAGGCAACTTAC 360
QY 361 TGATGGAGTGTGGAGCTCTCTAGATCTCAGGACCAACCGAGTGAACCTGTCTACTGTGTA 420
DB 361 TTATTGAAATGTGGAGCTCTCTAGATCTCAGGACCAACCGAGTGAACCTGTCTACTGTGTA 420
QY 421 GTACCTTTTGGAGAGCGGGAGTCTGGTGAACCGTTTCGAGCAGCAGCCTGTAAACGTTTG 480
DB 421 GTACCTTTTGGAGAGCGGGATTTCTGGTGACCGTTTGCAAAGCAGCACCCTGTAAACGTTTG 480

QY 481 TCAGAAATTTTCGCGGCTGGCTGAATTTTGAAGTGAAGCGGGGAAATGACAGAGCGTG 540
DB 481 TCAGAAATTTTCGCGGCTGGCTGAATTTTGAAGTGAAGCGGGGAAATGACAGAGCGTG 540
QY 541 ATTGGAAGACTAATGTACAGTCACTGTGGGCGCACTTGGGTGTGGTAAAGCAATGGG 600
DB 541 ATTGGAAGACTAATGTACAGTCACTGTGGGCGCACTTGGGTGTGGTAAAGCAATGGG 600
QY 601 CTGCTAAATTTTCGAGACCGGAAACACATCTGGAAACCACTAGAAACCAAGTGGTGG 660
DB 601 CTGCTAAATTTTCGAAACCCGAAACCACTAGAAACCACTAGAAACCAAGTGGTGG 660
QY 661 ATGGTTACCATGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGGCTGG 720
DB 661 ATGGTTACCATGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGGCTGG 720
QY 721 ATGATCTACTGAGACTGTGTGATCGATTCATTCATCTGTAGAGACTAAGGTGGACTG 780
DB 721 ATGATCTACTGAGACTGTGTGATCGATTCATTCATCTGTAGAGACTAAGGTGGACTG 780
QY 781 TACCTTTTTCGCGCGCAGTATTCTGATTACAGCAATCAGACCCCGTTGGAAATGGTACT 840
DB 781 TACCTTTTTCGCGCGCAGTATTCTGATTACAGCAATCAGACCCCGTTGGAAATGGTACT 840
QY 841 CCTCAACTGTCTGCCAGCTGTAGAGCTCTCTATCGAGAGTACTTCTCTGGTATTTT 900
DB 841 CCTCAACTGTCTGCCAGCTGTAGAGCTCTCTATCGAGAGTACTTCTCTGGTATTTT 900
QY 901 GGAAGAAATGCTACAGAAACATCCACGAGGAGGGGGCCAGTTCGTCAACCTTCCCGCC 960
DB 901 GGAAGAAATGCTACAGAAACATCCACGAGGAGGGGGCCAGTTCGTCAACCTTCCCGCC 960
QY 961 CATGCCCTGAATTTCCATATGAATTAATTAATCTAGTCTTTTATCACTTCGTAAATGGT 1020
DB 961 CATGCCCTGAATTTCCATATGAATTAATTAATCTAGTCTTTTATCACTTCGTAAATGGT 1020
QY 1021 TTTTATTTATTAATAAGG-TTAAGTGGGGGCTTTTAAATTAATTAATTTCTCTGAATTTA 1079
DB 1021 TTTTATTTATTAATAAGGTTTAAAGTGGGGGCTTTTAAAGTAAATTTCTCTGAATTTA 1080
QY 1080 CATACATGTTTACCGGATTTCTGTTCTGTATATCTATCTGTTTTCGAAAGCGAGTGC 1139
DB 1081 CATACATGTTTACCGGATTTCTGTTCTGTATATCTATCTGTTTTCGAAAGCGAGTGC 1140
QY 1140 CGAGGCTCTAGCTGTCTACATTTCCAGCAGTCTTGTAGTCTCAGCCACAGCTGGTCTTT 1199
DB 1141 CGAGGCTCTAGCTGTCTACATTTCTAGAGTCTTGTAGCTCAGCCAAAGCTGATTCCTTT 1200
QY 1200 TGTGTTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC 1259
DB 1201 TGTGTTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC 1260
QY 1260 GGGAGTGTAGGAGAGGCTGGGTATGTTATGGTGGCGGAGGAGTGTATACATAGGGGT 1319
DB 1261 GGGAGTGTAGGAGAGGCTGGGTATGTTATGGTGGCGGAGGAGTGTATACATAGGGGT 1320
QY 1320 CATAGGTGAGGCTGTGGCTTTGTATCAAAAGTATCATCTAAATTAAGCAGTCTGAGC 1379
DB 1321 CATAGGTGAGGCTGTGGCTTTGTATCAAAAGTATCATCTAGAAATAACAGAGTGGAGC 1380
QY 1380 CCATCCCTGTCAACCTGGGTGATCGGGGAGCAGGCGAGAAATTCACCTTAAACCTTTC 1439
DB 1381 CCATCCCTGTCAACCTGGGTGATCGGGGAGCAGGCGCAGAAATTCACCTTAAACCTTTC 1440
QY 1440 TTATTTCTGACTATTCAAAAGGCAACAGAGCGGGGTTTGAACCCCTCTCTGGGGAGAA 1499
DB 1441 TTATTTCTGACTATTCAAAAGGCAACAGAGGTTTGAAGTTTGGTCCCTCCCGGGGAA 1500
QY 1500 AGTCATTAATTAATCAATCTCATGTGCCCGCCAGGAGGGGCTTCTGACTGTGGTTC 1559
DB 1501 AGTCGTCAATTAATTAATCTCATGTGCCCGCCAGGAGGGGCTTGTGACTGTGGTAG 1560
QY 1560 GCTTGACAGTATATCCGAGGTCGGGAGAGGGGGTGTGTAAGATGCCATTTTTCCTTC 1619

Db 1561 CCTTGACAGTATATCCGAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTTCCTTC 1620
Qy 1620 TCCAGCGGTACGGTGGCGGGTGGAGCGCCAGCGGGCGGGGAGGATCGGCCAA 1679
Db 1621 TCCAAAGGTAGCGGTGGCGGGGTGGAGCGAGCGCGGGCGGGGAGGATCGGCCAA 1680
Qy 1680 GATGCTCGGGGGGGGTGTCTTCTTCTTGGTAAACGCTCTCGATACGTCATATCTG 1739
Db 1681 GATGCTCGGGGGGGGTGTCTTCTTCTCGGTAAACGCTCTCGATACGTCATATCTG 1740
Qy 1740 AAAACGAAAGAGTGGCTGTAAATTT 1767
Db 1741 AAAACGAAAGAGTGGCTGTAAATTT 1768

RESULT 6

US-09-347-594-1

; Sequence 1, Application US/09347594

; Patent No. 6217883

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon M.

; APPLICANT: MEEHAN, Brian M.

; APPLICANT: ELLIS, John A.

; APPLICANT: KRAKOWKA, George S.

; APPLICANT: AUDONNET, Jean-Christophe F.

; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE

; FILE REFERENCE: 454313-2338

; CURRENT APPLICATION NUMBER: US/09/347,594

; CURRENT FILING DATE: 1999-07-01

; EARLIER APPLICATION NUMBER: 98 08777

; EARLIER FILING DATE: 1998-07-06

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1767

; TYPE: DNA

; ORGANISM: Porcine circovirus

US-09-347-594-1

Query Match

Best Local Similarity 79.9%; Score 1412; DB 3; Length 1767;

Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGCGGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60
Db 348 ACCAGCGCACTTCGGCAGCGGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 407
Qy 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 120
Db 408 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 467
Qy 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATAATCCCTATTGTATTATTTA 180
Db 468 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATAATCCCTATTGTATTATTTA 527
Qy 181 TTGTTGGCAGGAGGTATGAGGAAGGAGCAACCTCACCTCCAGGGGTTCGCTAATT 240
Db 528 TTGTTGGCAGGAGGTATGAGGAAGGAGCAACCTCACCTCCAGGGGTTCGCTAATT 587
Qy 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTGTTGGGTGCCCGTCGCACATCG 300
Db 588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTGTTGGGTGCCCGTCGCACATCG 647
Qy 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATCTGCACTAAAGAGGCAACTTAC 360
Db 648 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATCTGCACTAAAGAGGCAACTTAC 707
Qy 361 TGATGGAGTGGAGTCTTCTAGATCTCAGGGAACACGGAGTGACCTGTCTGCTGTGA 420
Db 708 TGATGGAGTGGAGTCTTCTAGATCTCAGGGAACACGGAGTGACCTGTCTGCTGTGA 767
Qy 421 GTACCTTGTGGAGAGCGGGAGTCTGTTGACCGTTGACAGAGCAGCCCTGTAAACGTTTG 480

Db 768 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGACAGACCCCTGTAACTTTG 827
Qy 481 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATAATCAGAGCGTG 540
Db 828 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATAATCAGAGCGTG 887
Qy 541 ATTGGAAGACTAAATGTACACCTCATTTGTGGGGCCACCTGGGTGTGTTAAAGCAAAATGG 600
Db 888 ATTGGAAGACTAAATGTACACCTCATTTGTGGGGCCACCTGGGTGTGTTAAAGCAAAATGG 947
Qy 601 CTGCTAATTTTGCAGACCCGGAACCATACTCGAAACACCACTAGAAACCAAGTGGTGG 660
Db 948 CTGCTAATTTTGCAGACCCGGAACCATACTCGAAACCACTAGAAACCAAGTGGTGG 1007
Qy 661 ATGTTACCATGTGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGG 720
Db 1008 ATGTTACCATGTGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGG 1067
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCATTTGATGACTGTGAGAGCTAAAGTGAAC 780
Db 1068 ATGATCTACTGAGACTGTGTGATCGATATCATTTGATGACTGTGAGAGCTAAAGTGAAC 1127
Qy 781 TACCTTTTGGCCCGCAGTATCTGATTACCAATCAGACCCCGTTGGAATGCTACT 840
Db 1128 TACCTTTTGGCCCGCAGTATCTGATTACCAATCAGACCCCGTTGGAATGCTACT 1187
Qy 841 CCTCAACTGTCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 900
Db 1188 CCTCAACTGTCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 1247
Qy 901 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGCGAGTTCCTACCTTCCCTCC 960
Db 1248 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGCGAGTTCCTACCTTCCCTCC 1307
Qy 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCTGTAATG 1020
Db 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCTGTAATG 1367
Qy 1021 TTTTATTATTCAATTAAGGTTAAAGTGGGGGTCTTTAAATAATAAATTTCTCTGAATTTG 1080
Db 1368 TTTTATTATTCAATTAAGGTTAAAGTGGGGGTCTTTAAAGATTAATTTCTCTGAATTTG 1427
Qy 1081 ATACATGTTTACACGGAATATGTTATTCCTGTCGTATATACCTGTTTTCGAAACGAGTG 1140
Db 1428 ATACATGTTTACACGGAATATGTTATTCCTGTCGTATATACCTGTTTTCGAAACGAGTG 1487
Qy 1141 GAGGCTTACGTGCTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT 1200
Db 1488 GAGGCTTACGTGCTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT 1547
Qy 1201 GTTGTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTAC 1260
Db 1548 GTTGTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTAC 1607
Qy 1261 GGAGTGGTAGGAGAGGGCTGGGTTATGTTATGCGGGAGGAGTATGTTTACATAGGGGTC 1320
Db 1608 GGAGTGGTAGGAGAGGGCTGGGTTATGTTATGCGGGAGGAGTATGTTTACATAGGGGTC 1667
Qy 1321 ATAGTGGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
Db 1668 ATAGTGGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAGAAATAACAGCACTGGAGCC 1727
Qy 1381 CACTCCCTGTCACTCCCTGGTGCATCGGGGAGCAGGGGCCAG 1420
Db 1728 CACTCCCTGTCACTCCCTGGTGCATCGGGGAGCAGGGGCCAG 1767

RESULT 7

US-09-082-558-1

; Sequence 1, Application US/09082558A

; Patent No. 6368601

; GENERAL INFORMATION:

[illegible]

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PR 9800873
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PR 9803707
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PR 97/12382
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-161-092-1

Query Match 79.9%; Score 1412; DB 3; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGGCACTTCGGCAGCGGCGAGCACCCTCGGCGAGCAGCCTCAGCAGCAACATGCCCAGCA 60
DB 348 ACCAGGCACTTCGGCAGCGGCGAGCACCCTCGGCGAGCAGCCTCAGCAGCAACATGCCCAGCA 407

QY 61 AGAAGAAATGGAAGACGGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGAATAATC 120
DB 408 AGAAGAAATGGAAGACGGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGAATAATC 467

QY 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTATTTA 180
DB 468 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTATTTA 527

QY 181 TTGTGGCAGGAGGTATAGGAGGAGCAACACCTCACCTCCAGGGGTTTCGTAATT 240
DB 528 TTGTGGCAGGAGGTATAGGAGGAGCAACACCTCACCTCCAGGGGTTTCGTAATT 587

QY 241 TTGTGAAGACGAGACTTTTAATAAGTGAAGTGGTATTTGGGTGCCCCGCTGCCACATCG 300
DB 588 TTGTGAAGACGAGACTTTTAATAAGTGAAGTGGTATTTGGGTGCCCCGCTGCCACATCG 647

QY 301 AGAAGCGAAGGAAACAGATCAGCAGAAATAAGAAATPACTGCACTAAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGGAAACAGATCAGCAGAAATAAGAAATPACTGCACTAAAGAGGCAACTTAC 707

QY 361 TGATGAGTGTGAGACTCTAGATCTCAGGCAACCGAGTGACCTGTACTGTCTGTCGA 420
DB 708 TGATGAGTGTGAGACTCTAGATCTCAGGCAACCGAGTGACCTGTACTGTCTGTCGA 767

QY 421 GTACCTTTGAGAGCGGAGTCTGCTGACCGTTCAGAGCAGCACCTGTAAACGTTTG 480
DB 768 GTACCTTTGAGAGCGGAGTCTGCTGACCGTTCAGAGCAGCACCTGTAAACGTTTG 827

QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAATAATGCAAGCGGTG 540
DB 828 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAATAATGCAAGCGGTG 887

QY 541 ATTGGAAGACTAATATACGTCATTGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATATACGTCATTGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 947

QY 601 CTGCTAATTTTGCAGACCGGAAACCACTACTGGAACCCACCTAGAAACAACTGGTGGG 660
DB 948 CTGCTAATTTTGCAGACCGGAAACCACTACTGGAACCCACCTAGAAACAACTGGTGGG 1007

QY 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGCTGCCCTGGG 720
DB 1008 ATGGTTACCATGGTGAAGAGTGGTTGTTATGATGACTTTTATGGCTGCTGCCCTGGG 1067

QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTTAAGGTGGAACTG 780
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTTAAGGTGGAACTG 1127

QY 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

DB 1128 TACCTTTTTTGGCCCGCAGTATTCTGATTTACCACAATCAGACCCCGTTGGAATGGTACT 1187
QY 841 CCTCAACTGCTGCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 900
DB 1188 CCTCAACTGCTGCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 1247
QY 901 GGAAGAATGCTACAGAACAAATCCACGGAGGAAGGGGCGCAGTTGTCACCCCTTCCCGCCC 960
DB 1248 GGAAGAATGCTACAGAACAAATCCACGGAGGAAGGGGCGCAGTTGTCACCCCTTCCCGCCC 1307
QY 961 CATGCCCTGAATTTCCATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 1308 CATGCCCTGAATTTCCATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1367
QY 1021 TTTTATTATTCAATTAAGGTTAAAGTGGGGGCTCTTTAAAAATTAATTAATTAATTAATTAAT 1080
DB 1368 TTTTATTATTCAATTAAGGTTAAAGTGGGGGCTCTTTAAAAATTAATTAATTAATTAATTAAT 1427
QY 1081 ATACATGTTTACACGGATATTGTAATTCCTGCTGTATATATCTGTTTTCGAACGCAAGTCC 1140
DB 1428 ATACATGTTTACACGGATATTGTAATTCCTGCTGTATATATCTGTTTTCGAACGCAAGTCC 1487
QY 1141 GAGGCTACGTGCTTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200
DB 1488 GAGGCTACGTGCTTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1547
QY 1201 GTTGTTCGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260
DB 1548 GTTGTTCGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607
QY 1261 GGAGTGTAGGAGAGGCTGGGTTATGTTATGCGGAGGAGTAGTTTACATAGGGTTC 1320
DB 1608 GGAGTGTAGGAGAGGCTGGGTTATGTTATGCGGAGGAGTAGTTTACATAGGGTTC 1667
QY 1321 ATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
DB 1668 ATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAGAAATACAGCACTGGAGCC 1727
QY 1381 CACTCCCTGTCCACCCTGGGTGATCGGGAGGAGCGGCCAG 1420
DB 1728 CACTCCCTGTCCACCCTGGGTGATCGGGAGGAGCGGCCAG 1767

RESULT 9

US-09-583-350-1
; Sequence 1, Application US/09583350
; Patent No. 6517843
; GENERAL INFORMATION:
; APPLICANT: Ellis, et al.
; TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION A
; TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2
; FILE REFERENCE: 454313-2340.1
; CURRENT APPLICATION NUMBER: US/09/583,350
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/151,564
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-583-350-1

Query Match 79.9%; Score 1412; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGGCACTTCGGCAGCGGCGAGCACCCTCGGCGAGCAGCCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGGCACTTCGGCAGCGGCGAGCACCCTCGGCGAGCAGCCTCAGCAGCAACATGCCAGCA 407

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QY 61 AGAAGATGGAAGACGCGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 120
DB 408 AGAAGATGGAAGACGCGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 467
QY 121 CTTCCGAAGACGAGCGCAAGAAATAFACGGGATCTTCCAAATATCCCTATTTGATTATTTTA 180
DB 468 CTTCCGAAGACGAGCGCAAGAAATAFACGGGATCTTCCAAATATCCCTATTTGATTATTTTA 527
QY 181 TTGTTGGCGAGGAGGTAAATCAGGAGGACCAACACCTCACCTCCAGGGGTTCCTTAATT 240
DB 528 TTGTTGGCGAGGAGGTAAATCAGGAGGACCAACACCTCACCTCCAGGGGTTCCTTAATT 587
QY 241 TTGTGAAGACGACAGCTTTTAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
DB 588 TTGTGAAGACGACAGCTTTTAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 647
QY 301 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAAAGGCAACTTAC 360
DB 648 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAAAGGCAACTTAC 707
QY 361 TGATGGAGTGGAGCTCTAGATCTCAGGACCAACCGAGTGACCTGTCTACTGCTGTA 420
DB 708 TGATGGAGTGGAGCTCTAGATCTCAGGACCAACCGAGTGACCTGTCTACTGCTGTA 767
QY 421 GTACCTTTGGAGACGCGAGTCTGGTGACCGTTGCAGACGACACCTCTGAACGTTTG 480
DB 768 GTACCTTTGGAGACGCGAGTCTGGTGACCGTTGCAGACGACACCTCTGAACGTTTG 827
QY 481 TCAGAAATTTCCGGGGTGGCTGAACTTTTGAAGTGAAGGGAAGAAATGAGAAAGCGTG 540
DB 828 TCAGAAATTTCCGGGGTGGCTGAACTTTTGAAGTGAAGGGAAGAAATGAGAAAGCGTG 887
QY 541 ATTGAAGCACTAATGTACACGTCTATTTGGGGCCACCTGGTGTTGAAGCAAAATGGG 600
DB 888 ATTGAAGCACTAATGTACACGTCTATTTGGGGCCACCTGGTGTTGAAGCAAAATGGG 947
QY 601 CTGCTAAATTTGCAGACCGGAAACACATCTCTGAAACACCACTAGAAACAAAGTGGTGG 660
DB 948 CTGCTAAATTTGCAGACCGGAAACACATCTCTGAAACACCACTAGAAACAAAGTGGTGG 1007
QY 661 ATGGTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 1008 ATGGTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067
QY 721 ATGATCTACTGACCTGTGTGATCATATCCATTGACTGTAGAGACTAAAGTGAAGCTG 780
DB 1068 ATGATCTACTGACCTGTGTGATCATATCCATTGACTGTAGAGACTAAAGTGAAGCTG 1127
QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTACGAGCAATCAGACCCCGTTGGAATGGTACT 1187
QY 841 CTTCAACTGCTGTCCAGCTGTAGAAGCTCTTTTATCGGAGGATTAATCTTCTTGGTATTTT 900
DB 1188 CTTCAACTGCTGTCCAGCTGTAGAAGCTCTTTTATCGGAGGATTAATCTTCTTGGTATTTT 1247
QY 901 GGAAGATGCTACAGAAATATCCAGGAGGAGGGGGCCAGTTCGTACACCTTCCCGCCC 960
DB 1248 GGAAGATGCTACAGAAATATCCAGGAGGAGGGGGCCAGTTCGTACACCTTCCCGCCC 1307
QY 961 CATGCCCTGAATTTCCATATGAAATAAATTTACTGAGTCTTTTATCACTCTGTAATGGT 1020
DB 1308 CATGCCCTGAATTTCCATATGAAATAAATTTACTGAGTCTTTTATCACTCTGTAATGGT 1367
QY 1021 TTTTATTTATTAAGGTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGATC 1080
DB 1368 TTTTATTTATTAAGGTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGATC 1427
QY 1081 ATACATGGTTACCGGATTTGATTTCTGCTGCTATATCTGTTTTCGACGCGAGTGGC 1140
DB 1428 ATACATGGTTACCGGATTTGATTTCTGCTGCTATATCTGTTTTCGACGCGAGTGGC 1487
QY 1141 GAGGCTACGTGGTCTACATTTCCAGCAGTGTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200
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DB 1488 GAGGCCCTACGTGCTTACATTTCCAGCAGTGTGTAGTCTCAGCCACAGCTGGTTCTTTT 1547
QY 1201 GTTGTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGACAGGTTTGGGGGTAAGTACCG 1260
DB 1548 GTTGTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGACAGGTTTGGGGGTAAGTACCG 1607
QY 1261 GGAAGTGTAGGAGAGGGCTGGGTATGGTATGCGCGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1608 GGAAGTGTAGGAGAGGGCTGGGTATGGTATGCGCGGAGGAGTAGTTTACATAGGGGTC 1667
QY 1321 ATAGGTGAGGGCTGTGGCTTTGTTTCAAGTATATCATCTAAATTAACAGCCTCGAGCC 1380
DB 1668 ATAGGTGAGGGCTGTGGCTTTGTTTCAAGTATATCATCTAGAAATAACAGCCTCGAGCC 1727
QY 1381 CACTCCCTCTCACCTCGGTGATCGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTCTCACCTCGGTGATCGGGAGCAGGGCCAG 1767
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RESULT 10

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US-09-884-514-1
; Sequence 1, Application US/09884514
; Patent No. 6660272
; GENERAL INFORMATION:
; APPLICANT: MEEHAN, Gordon
; APPLICANT: ALLAN, Allan
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeilly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-1
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Query Match 79.9%; Score 1412; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 ACCAGCGCACTTCGGCAGCGCAGCACCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGGCAGCGCAGCACCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 407
QY 61 AGAAGATGGAAGACGCGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 120
DB 408 AGAAGATGGAAGACGCGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 467
QY 121 CTTCCGAAGACGAGCGCAAGAAATAFACGGGATCTTCCAAATATCCCTATTTGATTATTTTA 180
DB 468 CTTCCGAAGACGAGCGCAAGAAATAFACGGGATCTTCCAAATATCCCTATTTGATTATTTTA 527
QY 181 TTGTTGGCGAGGAGGTAAATCAGGAGGACCAACACCTCACCTCCAGGGGTTCCTTAATT 240
DB 528 TTGTTGGCGAGGAGGTAAATCAGGAGGACCAACACCTCACCTCCAGGGGTTCCTTAATT 587
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QY 241 TTGTGAAGAGCAGACTTTTAAATGAAGTGGTATTTGGTCCCGCTGCCACATCG 300
DB |||||
QY 588 TTGTGAAGAGCAGACTTTTAAATGAAGTGGTATTTGGTCCCGCTGCCACATCG 647
DB |||||
QY 301 AGAAGCGAAGGAACAGATCAGCAGATAAAGATCTGCGATGAAGAGCACTTAC 360
DB |||||
QY 648 AGAAGCGAAGGAACAGATCAGCAGATAAAGATCTGCGATGAAGAGCACTTAC 707
DB |||||
QY 361 TCAATGAGTGTGAGCTCTAGATCTCAGGGAACAACGGAGTCACTGTCTGTGTA 420
DB |||||
QY 708 TCAATGAGTGTGAGCTCTAGATCTCAGGGAACAACGGAGTCACTGTCTGTGTA 767
DB |||||
QY 421 GTACCTTTGTGAGAGCGGAGTCTGTGACCTTTGAGAGCAGACCTGTGTAAGCTTTG 480
DB |||||
QY 768 GTACCTTTGTGAGAGCGGAGTCTGTGACCTTTGAGAGCAGACCTGTGTAAGCTTTG 827
DB |||||
QY 481 TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATTCAGAGCGGTG 540
DB |||||
QY 828 TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATTCAGAGCGGTG 887
DB |||||
QY 541 ATTGGAAGACTAATGTACACGTCTTTGTGGGCGCACCTGGGTGTGTAAGCAATGGG 600
DB |||||
QY 888 ATTGGAAGACTAATGTACACGTCTTTGTGGGCGCACCTGGGTGTGTAAGCAATGGG 947
DB |||||
QY 601 CTGCTAATTTTGCAGACCGGGAACCACTACTGGAACCACTAGAAACCAAGTGGTGG 660
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QY 661 ATGTTACCATGTGAAGTGGTGTATTTGATGACCTTTTATGGCTGGCTGCCCTGGG 720
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QY 1008 ATGTTACCATGTGAAGTGGTGTATTTGATGACCTTTTATGGCTGGCTGCCCTGGG 1067
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QY 721 ATGATCTACTGAGCTGTGATCGATATCCATGCTGCTAGACGACTAAGTGGAGCTG 780
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QY 1068 ATGATCTACTGAGCTGTGATCGATATCCATGCTGCTAGACGACTAAGTGGAGCTG 1127
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QY 781 TACCTTTTGTGGCGCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGATGTACT 840
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QY 1128 TACCTTTTGTGGCGCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGATGTACT 1187
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QY 841 CCTCAACTGTCTCCAGCTGTAGAAAGCTTTTATCGGAGGATTAATCTCTGTGTAATTTT 900
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QY 1188 CCTCAACTGTCTCCAGCTGTAGAAAGCTTTTATCGGAGGATTAATCTCTGTGTAATTTT 1247
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QY 901 GGAAGATGCTACAGAAACCAATCCAGGAGGAGGGGGCGAGTTCGTCACCTTTCCCGCC 960
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QY 1248 GGAAGATGCTACAGAAACCAATCCAGGAGGAGGGGGCGAGTTCGTCACCTTTCCCGCC 1307
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QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTAATGGT 1020
DB |||||
QY 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTAATGGT 1367
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QY 1021 TTTTATTTATTCATTAAGGGTTAAGTGGGGCTTTTAAATTAATTAATCTCTGTAATGTAC 1080
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QY 1368 TTTTATTTATTCATTAAGGGTTAAGTGGGGCTTTTAAAGTAAATTAATCTCTGTAATGTAC 1427
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QY 1081 ATACATGGTTACAGGATTTATTTCTGGTGTATATCTGTTTTCGAGCCAGTGGC 1140
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QY 1428 ATACATGGTTACAGGATTTATTTCTGGTGTATATCTGTTTTCGAGCCAGTGGC 1487
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QY 1141 GAGGCTTACGTGTCTACATTTCCAGCAGTTTCTAGTCTCAGCAGACAGTGGTTTCTTTT 1200
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QY 1201 GTTGTGTTTGAAGTGAATCAATAGTGAATCTAGCAGAGTTTGGGGTGAAGTACCG 1260
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QY 1548 GTTGTGTTTGAAGTGAATCAATAGTGAATCTAGCAGAGTTTGGGGTGAAGTACCG 1607
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DB |||||
QY 1608 GAGTGTGTAAGAGGGCTGGGTATGTTATGCGGAGGAGTGTATTTACATAGGGTCT 1667
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QY 1321 ATAGGTGAGGGCTGTGGCCCTTTGTTACAAAGTTTATCATCTAAATTAACAGCACTGGAGCC 1380
DB |||||

DB 1668 ATAGGTGAGGGCTGTGGCTTTGTTTAAAGTTATCATCTAGAATAACAGCACTGGAGCC 1727
QY 1381 CACTCCCCCTGTCAACCTTGGGTGATCGGGGAGCAGGGCCAG 1420
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QY 1728 CACTCCCCCTGTCAACCTTGGGTGATCGGGGAGCAGGGCCAG 1767
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RESULT 11
US-09-347-594-2
; Sequence 2, Application US/09347594
; Patent No. 6217883
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon M.
; APPLICANT: MECHAN, Brian M.
; APPLICANT: ELLIS, John A.
; APPLICANT: KRAKOWKA, George S.
; APPLICANT: AUDONNET, Jean-Christophe F.
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE
; FILE REFERENCE: 454313-2338
; CURRENT APPLICATION NUMBER: US/09/347,594
; EARLIER FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: 98 08777
; EARLIER FILING DATE: 1998-07-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-347-594-2
Query Match 79.8%; Score 1410.4; DB 3; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACCAGCGCACTTTCGCGAGCGGCGAGCACTTCGCGAGCACTTCAGCAGCAACATGCCAGCA 60
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QY 348 ACCAGCGCACTTTCGCGAGCGGCGAGCACTTCGCGAGCACTTCAGCAGCAACATGCCAGCA 407
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QY 61 AGAAGAAATGGAGAGAGCGGACCCCAACCCCAATAAAGTGGGTGTTCACTCTGAATAATC 120
DB |||||
QY 408 AGAAGAAATGGAGAGAGCGGACCCCAACCCCAATAAAGTGGGTGTTCACTCTGAATAATC 467
DB |||||
QY 121 CTTCCGAAGAAGAGCGGCGCAAGAAATAACGGGATCTTCCCAATATCCCTATTTGATTTTAA 180
DB |||||
QY 468 CTTCCGAAGAAGAGCGGCGCAAGAAATAACGGGATCTTCCCAATATCCCTATTTGATTTTAA 527
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QY 181 TTGTTGGGAGAGGGGTATAGGAGAGCAACCACTCCTCAGGGGTTGCGTAAT 240
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QY 528 TTGTTGGGAGAGGGGTATAGGAGAGCAACCACTCCTCAGGGGTTGCGTAAT 587
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QY 241 TTGTTAGAGAGCAGACTTTTAAATGAAGTGGTATTTGGTGGCCGCTGCCACATCG 300
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QY 588 TTGTTAGAGAGCAGACTTTTAAATGAAGTGGTATTTGGTGGCCGCTGCCACATCG 647
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QY 828 TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATTCAGAGCGGTG 887
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QY 541 ATTGGAAGACTAATGTACACGTCTTTGTTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
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Qy 661 ATGTTTACCATGGTGAAGAAGTGGTGTATATGAGTCTTTTATGAGTCTGGTGGTGGTGGG 720
Db 1008 ATGTTTACCATGGTGAAGAAGTGGTGTATATGAGTCTTTTATGAGTCTGGTGGTGGTGGG 1067
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Db 1068 ATGATCTACTGAGACTGTGTATCATATCATCTGAGTCTGAGACTTAAAGTGGAACTG 1127
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Db 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 1187
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Db 1188 CCTCAACTGCTGCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTTCCCTTGGTATTTT 1247
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Qy 1321 ATAGGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCACTGAGCC 1380
Db 1668 ATAGGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCACTGAGCC 1727
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Db 1728 CACTCCCTGTCACTCCCTGCTGATCGGGGAGCAGGSCCAG 1767
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RESULT 12

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US-09-082-558-2
; Sequence 2, Application US/09082558A
; Patent No. 638601
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
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; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/082,558A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: FR 9800873
; EARLIER FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: FR 9803707
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: FR 97/12382
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
; US-09-082-558-2

Query Match 79.8%; Score 1410.4; DB 3; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGCGCGCAGCACCTCGGAGCAGCACTTCAGCAGCAACATGCCAGCA 60
Db 348 ACCAGCGCACTTCGGCAGCGCGCAGCACCTCGGAGCAGCACTTCAGCAGCAACATGCCAGCA 407
Qy 61 AGAAGATGAAGAGCGGACCCCAACCCCATAAAGTGGTGGTTCACCTCTCAATTAATC 120
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Qy 121 CTTCCGAAGACGAGCGCAAGAAATACGGATCTTCCAATATCCCTATTTGATTTTAA 180
Db 468 CTTCCGAAGACGAGCGCAAGAAATACGGATCTTCCAATATCCCTATTTGATTTTAA 527
Qy 181 TTGTTGGCAGAGGGTAAATGAGAGGAGCAACACCTCACTCCAGGGGTTGGCTAATT 240
Db 528 TTGTTGGCAGAGGGTAAATGAGAGGAGCAACACCTCACTCCAGGGGTTGGCTAATT 587
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Db 648 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTCAGTAAAGAGGCAACTTAC 707
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Db 708 TGATGGAGTGTGAGTCTTAGATCTCAGGACCAACGGAGTACCTCTCTACTCTCTGA 767
Qy 421 GTACCTTTGGAGAGCGGGAGTCTGGTGAACCGTTGAGAGCAGCAGCACCTGTAACTGTTG 480
Db 768 GTACCTTTGGAGAGCGGGAGTCTGGTGAACCGTTGAGAGCAGCAGCACCTGTAACTGTTG 827
Qy 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
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Qy 541 ATTGGAAGACTAATGTACAGCTCATTTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
Db 888 ATTGGAAGACTAATGTACAGCTCATTTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 947
Qy 601 CTGCTAATTTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 660
Db 948 CTGCTAATTTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 1007
Qy 661 ATGTTTACCATGGTGAAGAAGTGGTGTATATGAGTCTTTTATGAGTCTGGTGGTGGTGGG 720
Db 1008 ATGTTTACCATGGTGAAGAAGTGGTGTATATGAGTCTTTTATGAGTCTGGTGGTGGTGGG 1067
Qy 721 ATGATCTACTGAGACTGTGTATCATATCATCTGAGTCTGAGACTTAAAGTGGAACTG 780
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1068	ATGATCTACTGAGACTGTGTATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACTG	1121
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1128	TACCTTTTGGCCCGCAGTATTCTGAATACCAAGCAATCAGACCCCGTTGGAATGGTACT	1187
841	CCTCAACGTGTCGCCAGCTGTAGAAGCTCTTTATCGGAGGATTTACTTTCCTTGATTTTT	900
1188	CCTCAACTGCTGTCCCAAGCTGTAGAAGCTCTTTATCGGAGGATTTACTTTCCTTGATTTTT	1247
901	GSAAAGATGCTACAGAAACAATCCA CGGAGGAAGGGGCCAGTTTCGTCAACCTTTCCCCCC	960
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1308	CATGCCCTGAATTTCCATATGAATAAATTAATCTAGAGTCTTTTTTATCACTTCGTAATGGT	1367
1021	TTTTTATTATTCAATTAAGGGTTAAGTGGGGGTCTTTAAAAATTAATTTCTCTGAATCTGAC	1080
1368	TTTTTATTATTCAATTAAGGGTTAAGTGGGGGTCTTTAAGATTAAATTTCTCTGAATCTGAC	1427
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1321	ATAGGTGAGGGCTGTGGCCCTTTGTTTCAAAAGTATCATCTAAAAATAACAGACACTGGAGCC	1380
1568	ATAGGTGAGGGCTGTGGCCCTTTGTTTCAAAAGTATCATCTAGAATAACAGACACTGGAGCC	1727
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RESULT 13

RES001 13
US-09-161-092-2
; Sequence 2, Application US/09161092
; Patent No. 6391314
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/161,092
; CURRENT FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03

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Qy 1021 TTTTATTATTCAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTTCTCTGAATTTGAC 1080
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Qy 1081 ATACATGGTTACAGGATATTTGATTTCTGTCGTATATCTGTTTTCGAACGAGTGGCC 1140
Db 1428 ATACATGGTTACAGGATATTTGATTTCTGTCGTATATCTGTTTTCGAACGAGTGGCC 1487
Qy 1141 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCACAGTGGTTCCTTTT 1200
Db 1488 GAGGCTACGTGGTCTACATTTCCAGTGTGTTAGTCTCAGCCACAGTGAATTTCTTTT 1547
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Db 1608 GGAGTGTAGGAGAGGGCTGGTTATGTTATGCGGAGGAGGAGTAGTTTACATAGGGTTC 1667
Qy 1321 ATAGGTAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
Db 1668 ATAGGTAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1727
Qy 1381 CACTCCCTGTCACTCCCTGGTGTATGCGGAGGAGGAGGAGCCAG 1420
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RESULT 14
US-09-583-350-2
; Sequence 2, Application US/09583350
; Patent No. 6517843
; GENERAL INFORMATION:
; APPLICANT: Ellis, et al.
; TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION AS
; FILE REFERENCE: 454313-2340.1
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/151,564
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-583-350-2

Query Match 79.8%; Score 1410.4; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACCAGCGCATCTCGGAGGCGGAGCACCTCGGAGCACCTCAGCAGCAACATGCCCGAGCA 60
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Qy 1261 GGAGTGTAGGAGAGGGCTGGTTATGTTATGCGGAGGAGGAGGAGCCAG 1320
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Db 1608 CGAGTGTAGGAGAGGCTGGTGTATGGTATGGCGGAGGAGTAGTTTACATAGGGTC 1667
Qy 1321 ATAGGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
Db 1668 ATAGGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAGAAATACAGCACTGGAGCC 1727
Qy 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1420
Db 1728 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1767

RESULT 15
US-09-884-514-2
; Sequence 2, Application US/09884514
; Patent No. 6660272
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeilly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-2

Query Match 79.8%; Score 1410.4; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGCGGAGCAGCACCTCGGAGCAGCACCTCAGCAGCAACATGCCAGCA 60
Db 348 ACCAGCGCACTTCGGCAGCGGAGCAGCACCTCGGAGCAGCACCTCAGCAGCAACATGCCAGCA 407
Qy 61 AGAAGAAATGGAAGAGCGGAGCCCAACCCCATAAAGTGGGTGTTCACTCTGAATAATC 120
Db 408 AGAAGAAATGGAAGAGCGGAGCCCAACCCCATAAAGTGGGTGTTCACTCTGAATAATC 467
Qy 121 CTTCCGAGAGCAGGCGCAAGAAATAACGGATCTTCCAATATCCCTATTGATTATTTTA 180
Db 468 CTTCCGAGAGCAGGCGCAAGAAATAACGGATCTTCCAATATCCCTATTGATTATTTTA 527
Qy 181 TTGTTCCGAGGAGGCTAATGAGGAGGAGCAACCTCACCTCCAGGGGTTTCGCTAAAT 240
Db 528 TTGTTCCGAGGAGGCTAATGAGGAGGAGCAACCTCACCTCCAGGGGTTTCGCTAAAT 587
Qy 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGTGC CGCTGCCACATCG 300
Db 588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGTGC CGCTGCCACATCG 647
Qy 301 AGAAGCGAAGGAAACAGATACAGCAAAATAAGAAATATCTGAGTAAGAGGCAACTTAC 360
Db 648 AGAAGCGAAGGAAACAGATACAGCAAAATAAGAAATATCTGAGTAAGAGGCAACTTAC 707

Qy 361 TGATGGAGTGTGGAGCTCTTAGATCTCAGGGAACAACGAGTGACCTGTCTACTGCTGTGA 420
Db 708 TGATGGAGTGTGGAGCTCTTAGATCTCAGGGAACAACGAGTGACCTGTCTACTGCTGTGA 767
Qy 421 GTACCTTGTTCGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG 480
Db 768 GTACCTTGTTCGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG 827
Qy 481 TCAGAAATTTCCGGGGCTGGCTGAATTTTGAAGTGAAGGGAAGTAAAGCAAGACGTCG 540
Db 828 TCAGAAATTTCCGGGGCTGGCTGAATTTTGAAGTGAAGGGAAGTAAAGCAAGACGTCG 887
Qy 541 ATTGGAAGACTAATGTATACAGCTCATTTGTTGGGGCCACCTGGGTGTGGTAAAGCAATGG 600
Db 888 ATTGGAAGACTAATGTATACAGCTCATTTGTTGGGGCCACCTGGGTGTGGTAAAGCAATGG 947
Qy 601 CTGCTAATTTTGCAGAGCCCGGAACCAATCTGGAACACCACTAGAAACAAAGTGGTGG 660
Db 948 CTGCTAATTTTGCAGAGCCCGGAACCAATCTGGAACACCACTAGAAACAAAGTGGTGG 1007
Qy 661 ATGTTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGG 720
Db 1008 ATGTTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGG 1067
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCAATGACTGTAGAGACTAAAGTGGAACTG 780
Db 1068 ATGATCTACTGAGACTGTGTGATCGATATCAATGACTGTAGAGACTAAAGTGGAACTG 1127
Qy 781 TACCTTTTGGCCCGCAGTATTCGATTACCAGCAATCAGACCCCTGGGAATGGTACT 840
Db 1128 TACCTTTTGGCCCGCAGTATTCGATTACCAGCAATCAGACCCCTGGGAATGGTACT 1187
Qy 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTCTGGTATTTT 900
Db 1188 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTCTGGTATTTT 1247
Qy 901 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGGCAGTTCGTACCCCTTCCCCC 960
Db 1248 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGGCAGTTCGTACCCCTTCCCCC 1307
Qy 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTAATGCT 1020
Db 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTAATGCT 1367
Qy 1021 TTTTATTTATTAAGGTTAAAGTGGGGGCTCTTTAAATTAATTTCTCTGAATTTGTAC 1080
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Qy 1081 ATACATGTTTACACGGATATTGTATTCGTGGTCGTATATACATCTGTTTTCGAACGCACTGCC 1140
Db 1428 ATACATGTTTACACGGATATTGTATTCGTGGTCGTATATACATCTGTTTTCGAACGCACTGCC 1487
Qy 1141 GAGGCTAGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
Db 1488 GAGGCTAGTGGTCTACATTTCCAGTGTGTGTAGTCTCAGCCACAGCTGTATTTCTTTT 1547
Qy 1201 GTTGTGTTGGTTCGAAGTAAATCAATAGTGAATCTAGGACAGGTTGGGGGTAAAGTACC 1260
Db 1548 GTTGTGTTGGTTCGAAGTAAATCAATAGTGAATCTAGGACAGGTTGGGGGTAAAGTACC 1607
Qy 1261 GGAGTGTAGGAGAGGGCTGGTGTATGGTATGGCGGAGGAGTGTATTCATAGGGGTC 1320
Db 1608 GGAGTGTAGGAGAGGGCTGGTGTATGGTATGGCGGAGGAGTGTATTCATAGGGGTC 1667
Qy 1321 ATAGGTAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGAGCC 1380
Db 1668 ATAGGTAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAGAAATACAGCACTGAGCC 1727
Qy 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1420
Db 1728 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1767

Wed Dec 8 12:30:21 2004

us-10-718-264-15.rni

Page 16

Search completed: December 7, 2004, 20:05:45
Job time : 160 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:33:09 ; Search time 877 seconds
(without alignments)

10576.656 Million cell updates/sec

Title: US-10-718-264-15

Perfect score: 1767

Sequence: 1 accagcgacttcggcagc.....agaagtcgctgaagtatt 1767

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645.6	93.1	1768	2 AAX83754	Aax83754 Porcine c
2	1642.4	92.9	1768	4 AAF75841	Aaf75841 PCV DNA f
3	1636.8	92.6	1768	4 AAF75840	Aaf75840 PCV DNA f
4	1620	91.7	1768	8 ABV72527	Abv72527 Nucleotid
5	1545.4	87.5	1786	2 AAX83755	Aax83755 Porcine c
6	1412	79.9	1767	2 AAX35378	Aax35378 Nucleotid
7	1412	79.9	1767	2 AAX35210	Aax35210 Nucleotid
8	1412	79.9	1767	3 AAF25689	Aaz56869 DNA seque
9	1412	79.9	1767	4 AAF75835	Aaf75835 PCV DNA f
10	1410.4	79.8	1767	2 AAX35379	Aax35379 Nucleotid
11	1410.4	79.8	1767	2 AAX35211	Aax35211 Nucleotid
12	1410.4	79.8	1767	3 AAZ56870	Aaz56870 DNA seque
13	1410.4	79.8	1767	4 AAF75836	Aaf75836 PCV DNA f
14	1335.4	75.6	1768	2 AAX35381	Aax35381 Nucleotid
15	1335.4	75.6	1768	2 AAX35380	Aax35380 Nucleotid
16	1335.4	75.6	1768	2 AAX35213	Aax35213 Nucleotid
17	1335.4	75.6	1768	2 AAX35212	Aax35212 Nucleotid
18	1335.4	75.6	1768	3 AAZ56872	Aaz56872 DNA seque
19	1335.4	75.6	1768	3 AAZ56871	Aaz56871 DNA seque
20	1335.4	75.6	1768	4 AAF75837	Aaf75837 PCV DNA f
21	1335.4	75.6	1768	4 AAF75838	Aaf75838 PCV DNA f

ALIGNMENTS

RESULT 1

AAX83754
ID AAX83754 standard; DNA; 1768 BP.

AC AAX83754;

DT 27-AUG-1999 (first entry)

DE Porcine circovirus type II 412 nucleotide sequence.

KW Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;
KW postweaning multisystemic wasting syndrome virus; diagnosis; ds.

OS Porcine circovirus.

PN WO9929717-A2.

PD 17-JUN-1999.

PF 11-DEC-1998; 98WO-CA001130.

PR 11-DEC-1997; 97US-0069233P.

PR 16-DEC-1997; 97US-0069750P.

XX (UWSA-) UNIV SASKATCHEWAN.

PI Wang L, Babiuk LA, Potter AA, Willson P;

DR WPI; 1999-394957/33.

PT New isolated porcine circovirus Type II.

PS Claim 1; Fig 2; 82pp; English.

CC The present invention describes a new isolated porcine circovirus Type II (PCVII), obtained from postweaning multisystemic wasting syndrome-affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide sequences. AAY24929 to AAY24934 represent PCVII open reading frame (ORF) proteins (N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not correspond exactly with the PCVII ORFs given in Fig 3A to Fig 3D). The PCVII polypeptides can be used for treating or preventing PCVII infection in vertebrates. The products can also be used to detect the PCVII

SQ Sequence 1768 BP; 454 A; 361 C; 492 G; 461 T; 0 U; 0 Other;

22	1324.6	75.0	1768	2	AAX35382	Aax35382 Nucleotid
23	1324.6	75.0	1768	2	AAX35012	Aax35012 Genomic D
24	1324.6	75.0	1768	2	AAX35214	Aax35214 Nucleotid
c 25	1176.4	66.6	1768	9	AAL57176	Aal57176 Porcine c
26	1144.4	64.8	1361	2	AAX83757	Aax83757 Porcine c
27	1005.6	56.9	1759	2	AAX85593	Aax85593 Nucleotid
28	1000.8	56.6	1759	2	AAX87992	Aax87992 Porcine c
29	920.8	52.1	3609	4	AAF28320	Aaf28320 PJPI07 do
c 30	890.6	50.4	1759	2	AAX35013	Aax35013 Nucleotid
31	886.4	50.2	1759	4	AAF75839	Aaf75839 DNA fragm
32	866.4	49.0	1768	6	ABX08205	Abx08205 PMWS-Porc
33	864.8	48.9	1768	6	ABX08207	Abx08207 CT-Porc
34	863.2	48.9	1768	6	ABX08206	Abx08206 CT-Porc
35	863.2	48.9	1768	6	ABX08204	Abx08204 PMWS-Porc
36	860	48.7	1768	6	ABX08203	Abx08203 PMWS-Porc
37	856.8	48.5	1774	6	ABX08219	Abx08219 PMWS-Porc
38	841.2	47.6	1762	6	ABX08202	Abx08202 PMWS-Porc
39	741.8	42.0	5285	4	AAH74865	Aah74865 Nucleotid
40	741.8	42.0	5285	8	ABX94355	Abx94355 Rolling c
41	741.8	42.0	5650	4	AAH74866	Aah74866 Nucleotid
42	741.8	42.0	5650	8	ABX94356	Abx94356 Rolling c
43	719.4	40.7	7460	4	AAH74867	Aah74867 Nucleotid
44	719.4	40.7	7460	8	ABX94361	Abx94361 Rolling c
c 45	674.8	38.2	1773	9	AAL57177	Aal57177 Porcine c

Query Match		93.1%; Score 1645.6; DB 2; Length 1768;
Best Local Similarity		96.0%; Pred. No. 0;
Matches 1698; Conservative		0; Mismatches 69; Indels 1; Gaps 1;
Qy	1	ACGAGCCACTTCGGCAGCGCAGCAGCTCGGACGACCTCAGCAGCAACATGCCAGCA 60
Db	1	ACGAGCCACTTCGGCAGCGCAGCAGCTCGGACGACCTCAGCAGCAACATGCCAGCA 60
Qy	61	AGAAAGATGGAAGAGCGGACCCCAACCCCAATAAAAGTGGGTTCACCTCGAATAATC 120
Db	61	AGAAAGATGGAAGAGCGGACCCCAACCCCAATAAAAGTGGGTTCACCTCGAATAATC 120
Qy	121	CTTCGGAAGACGAGCGCAAGAAATACGGGATCTCCCAATATCCCTATTTGATTTTAA 180
Db	121	CTTCGGAAGACGAGCGCAAGAAATACGGGATCTCCCAATATCCCTATTTGATTTTAA 180
Qy	181	TTGTTGGCGAGGAGGTAAATGAGGAGGACCAACACCTCACCTCAGGGGTTCGCTAAT 240
Db	181	TTGTTGGCGAGGAGGTAAATGAGGAGGACCAACACCTCACCTCAGGGGTTCGCTAAT 240
Qy	241	TTGTGAAGACGACATTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Db	241	TTGTGAAGACGACATTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Qy	301	AGAAAGCGAAAGGACAGATCAGCAGAAATGAAGTACTGCACTAAGAGGCAACTTAC 360
Db	301	AGAAAGCGAAAGGACAGATCAGCAGAAATGAAGTACTGCACTAAGAGGCAACTTAC 360
Qy	361	TGATGGAGTGTGAGCTCTAGATCTCAGGGAACACGAGTCACTGTCTACTCTGTGA 420
Db	361	TTATTTGAATGTGAGCTCTCGATCTCAAGGACACGAGTGACCTGTCTACTCTGTGA 420
Qy	421	GTACCTTGTGTGAGAGCGGAGTCTGTGAGCCGTTGACAGAGCAGCACCCTGTACGTTG 480
Db	421	GTACCTTGTGTGAGAGCGGAGTCTGTGAGCCGTTGACAGAGCAGCACCCTGTACGTTG 480
Qy	481	TCGAAATTTCCGGCGGTGGCTGAATTTTGAAGTGAAGGAGGAGGAGGAGGAGGAGG 540
Db	481	TCGAAATTTCCGGCGGTGGCTGAATTTTGAAGTGAAGGAGGAGGAGGAGGAGGAGG 540
Qy	541	ATTGGAAGACTAATGTACAGCTCATTTGGGGCCACCTGGGTGGTGAAGAAATGGG 600
Db	541	ATTGGAAGACTAATGTACAGCTCATTTGGGGCCACCTGGGTGGTGAAGAAATGGG 600
Qy	601	CTGCTAATTTGAGACCCGGAACCAATCTGGAACCCACTAGAACCAAGTGGTGGG 660
Db	601	CTGCTAATTTGAGACCCGGAACCAATCTGGAACCCACTAGAACCAAGTGGTGGG 660
Qy	661	ATGGTTACCATGTGGAAGAGTGGTGTATTTGATGACCTTTATGGCTGGCTGCCCTGGG 720
Db	661	ATGGTTACCATGTGGAAGAGTGGTGTATTTGATGACCTTTATGGCTGGCTGCCCTGGG 720
Qy	721	ATGATCTACTGAGCTGTGTGATCGATATCCATTTGATGAGTATGAGTAAAGTGAATCTG 780
Db	721	ATGATCTACTGAGCTGTGTGATCGATATCCATTTGATGAGTATGAGTAAAGTGAATCTG 780
Qy	781	TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTGGTGAATGTACT 840
Db	781	TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTGGTGAATGTACT 840
Qy	841	CCTCAACTGTGTCGCCAGCTAGAAAGCTCTTTATCGAGGATTAATCTCTTGGTATTTT 900
Db	841	CCTCAACTGTGTCGCCAGCTAGAAAGCTCTTTATCGAGGATTAATCTCTTGGTATTTT 900
Qy	901	GGAAGAAATGCTACAGAAATCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db	901	GGAAGAAATGCTACAGAAATCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy	961	CATGCCCTGAATTTCCATATGAATAAATTTACTGAGTCTTTTTTATCACTTCGTATGGT 1020
Db	961	CATGCCCTGAATTTCCATATGAATAAATTTACTGAGTCTTTTTTATCACTTCGTATGGT 1020

Qy	1021	TTTTATTATTCAATTAAGGGTT-AAAGTGGGGGTCTTTAAAAATTAATTTCTCTGAATTGTA 1079
Db	1021	TTTTATTATTCAATTAAGGGTTCAAGTGGGGGTCTTTAAAGATTAATTTCTCTGAATTGTA 1080
Qy	1080	CATA CATGGTTACACGGATATTTGATTTCTCTGGTGGTATATCTGTTTTCGAAACGAGTGC 1139
Db	1081	CATACATGGTTACACGGATATTTGATTTCTCTGGTGGTATTTTACTGTTTTCGAAACGAGTGC 1140
Qy	1140	CGAGGCTACGTTGGTCTCATTTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTT 1199
Db	1141	CGAGGCTACGTTGGTCTCCATTTTCCAGAGTTTGTAGCTCAGCCAAAGCTGATTCCTTT 1200
Qy	1200	TGTTGTTTGGTGGAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC 1259
Db	1201	TGTTATTTGGTGGAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260
Qy	1260	GGAGTGTAGAGAGGGCTGGTATGTTATGTTGCGGGAGGAGTAGTTTACATAGGGGT 1319
Db	1261	GGAGTGTAGAGAGGGTGGGATTTGGGGATTTGTTGCGGGAGGAGTAGTTTACATAGGGT 1320
Qy	1320	CATAGTGAAGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAAAATAACAGCACTGGAGC 1379
Db	1321	CATAGTGAAGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAAAATAACAGCACTGGAGC 1380
Qy	1380	CCACTCCCTGTCA CCGTGGGTATCGGGAGCAGGGCCAGAAATTCACCTTAACTTTTC 1439
Db	1381	CCACTCCCTATCACCTGGGTGATGGGGAGCAAGGCCAGAAATTCACCTTAACTTTTC 1440
Qy	1440	TTATTTCTGTAGTATTTCAAGAGGCACAGAGCGGGGTTTACCCCCCTCTCGGGGGAAGAA 1499
Db	1441	TTATTTCTGTAGTATTTCAAGAGGTATAGAGATTTTGTGTTGTTCCCTCCCGGGGAACAA 1500
Qy	1500	AGTCATTAAATTAATTTCTCATCATGTCCACCGCCAGAGGGCGTTCTGACTGTGGTTC 1559
Db	1501	AGTCGTAATTTTAAATTTCTCATCATGTCCACCGCCAGAGGGCGTTGTGACTGTGGTAC 1560
Qy	1560	GCTTGACAGTATATCCGAGGTGCGGAGGCGGTGTTGAAGTGCATTTTCTCTTC 1619
Db	1561	GCTTGACAGTATATCCGAGGTGCGGAGGCGGTGTTGAAGTGCATTTTCTCTTC 1620
Qy	1620	TCCAGCGGTAAACGGTGGCGGGGTGACAGCCAGCGGGCGGGCGGAGGATCTGCCCAA 1679
Db	1621	TCCAAACGTTAGCGGTGGCGGGGTGACAGCCAGCGGGCGGGCGGAGGATCTGCCCAA 1680
Qy	1680	GATGGCTGCGGGCGGCGGTCTTCTTCTTCGGTAAACGCTCTTGGATAGCTCATATCTG 1739
Db	1681	GATGGCTGCGGGCGGCGGTCTTCTTCTGCGGTAAACGCTCTTGGATAGCTCATATCTG 1740
Qy	1740	AAAAACGAAAGTGGCTGTAAAGTATT 1767
Db	1741	AAAAACGAAAGTGGCTGTAAAGTATT 1768

RESULT 2

AAF75841 standard; DNA; 1768 BP.

AC AAF75841;
XX

DT 06-AUG-2003 (revised)
DT 18-MAY-2001 (first entry)

PF 28-AUG-2000; 2000WO-EP008781.
XX
PR 31-AUG-1999; 99US-0151564P.
PR 31-MAY-2000; 2000US-00583350.
XX
XX (MERI-) MERIAL.
PA (UYSA-) UNIV SASKATCHEWAN.
PA (UYBE-) UNIV QUEBENS BELFAST.
XX
XX Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;
PI Harding J, Charreyre CB, Chappuis GE, Krakowka GS, Audonnet JF;
PI Mcneilly F;
XX
DR WPI; 2001-244408/25.
XX
XX Use of porcine circovirus-2 immunogen to formulate a vaccine composition
PT to treat pigs against myocarditis, abortion, intrauterine infection
PT and/or post-weaning, multisystemic wasting syndrome associated with PCV-
PT 2.
XX
XX Claim 11; Fig 7; 134pp; English.
XX
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)
CC immunogen to formulate a vaccine composition to prevent or treat pigs
CC against myocarditis and/or abortion and/or intrauterine infection and/or
CC post-weaning, multisystemic wasting syndrome and other pathological
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of
CC a strain of PCV, which was used in the present invention. (Updated on 06-
CC AUG-2003 to correct OS field.)
XX
XX Sequence 1768 BP; 452 A; 359 C; 496 G; 461 T; 0 U; 0 Other;
SQ

Query Match 92.9%; Score 1642.4; DB 4; Length 1768;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 ACCAGCGACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60
DB 1 ACAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60

QY 61 AGAAGATGAAGAAGCGGACCCCAACCCCATAAAGGTGGGTCTACTCTGAATAATC 120
DB 61 AGAAGATGAAGAAGCGGACCCCAACCCCATAAAGGTGGGTCTACTCTGAATAATC 120

QY 121 CTTCCGACAGCAGCAAGAAATACCGGATCTTCCATATCCCTATTTGATTTTAA 180
DB 121 CTTCCGACAGCAGCAAGAAATACCGGATCTTCCATATCCCTATTTGATTTTAA 180

QY 181 TTGTTGGCGAGGAGGTAATGAGGAGGAGCAACACCTCACCTCCAGGGGTTCGCTAAT 240
DB 181 TTGTTGGCGAGGAGGTAATGAGGAGGAGCAACACCTCACCTCCAGGGGTTCGCTAAT 240

QY 241 TTGTGAAGAAGCAGACTTTTAAATGAAGTGGTATTTGGGTGCCGCTGCCACATCG 300
DB 241 TTGTGAAGAAGCAGACTTTTAAATGAAGTGGTATTTGGGTGCCGCTGCCACATCG 300

QY 301 AGAAGCGAAGAAAGACAGATCAGCAGAAATAGAGATATCGCAGTAAGAGGCAACTTAC 360
DB 301 AGAAGCGAAGAAAGACAGATCAGCAGAAATAGAGATATTTGCAGTAAGAGGCAACTTAC 360

QY 361 TGATGAGGTGGAGCTCTAGATCTCAGGCAACCGAGTGACCTGTCTACTGTGTGA 420
DB 361 TTATTGAATGTGGAGCTCTCTGATCTCAAGGACACCGAGTGACCTGTCTACTGTGTGA 420

QY 421 GTACCTTTGTGAGAGCGGAGTCTGGTGAACCGTTGCAGAGCAGCAACCTGTAACTTTG 480
DB 421 GTACCTTTGTGAGAGCGGAGTCTGGTGAACCGTTGCAGAGCAGCAACCTGTAACTTTG 480

QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGCAGCGGAAATGCAGAGCGTG 540
DB 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGCAGCGGAAATGCAGAGCGTG 540

QY 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
DB 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600
QY 601 CTGCTAATTTTGCAGACCCCGAAACACATACTGGAACACACCTTAGAAGTGGTGGG 660
DB 601 CTGCTAATTTTGCAGACCCCGAAACACATACTGGAACACACCTTAGAAGTGGTGGG 660
QY 661 ATGGTTACCATGTGTGAAGAGTGGTGTATTAATGAATCTTTATGGCTGGCTGGCTGG 720
DB 661 ATGGTTACCATGTGTGAAGAGTGGTGTATTAATGAATCTTTATGGCTGGCTGGCTGG 720
QY 721 ATGATCTACTGAGACTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAACGTG 780
DB 721 ATGATCTACTGAGACTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAACGTG 780
QY 781 TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTGGTGAATGGTACT 840
DB 781 TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTGGTGAATGGTACT 840
QY 841 CCTCAACTGTGTCCAGCTGTAGAAGCTCTTTATCGAGGATTAATCTCTTGGTATTTT 900
DB 841 CCTCAACTGTGTCCAGCTGTAGAAGCTCTTTATCGAGGATTAATCTCTTGGTATTTT 900
QY 901 GGAAGATGCTACAGAAATCCACGAGGAGGAGGCGCAGTTCGTCAACCTTTCCCGCC 960
DB 901 GGAAGATGCTACAGAAATCCACGAGGAGGAGGCGCAGTTCGTCAACCTTTCCCGCC 960
QY 961 CATGCCCTGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
DB 961 CATGCCCTGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
QY 1021 TTTTATTATTCA - TTAAGGGTTAAGTGGGGTCTTTAAATTAATTAATTAATTAATTAATTA 1079
DB 1021 TTTTATTATTCA - TTAAGGGTTAAGTGGGGTCTTTAAATTAATTAATTAATTAATTAATTA 1080
QY 1080 CATACATGTTTACAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1139
DB 1081 CATACATGTTTACAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
QY 1140 CGAGCCTTACGTTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACACAGCTGGTTCTTT 1199
DB 1141 CGAGCCTTACGTTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACACAGCTGGTTCTTT 1200
QY 1200 TGTGTTTGGTGGAAAGTAAATCAATAGTGAATCTAGACAGGTTGGGGTGAAGTACC 1259
DB 1201 TGTGTTTGGTGGAAAGTAAATCAATAGTGGAGTCAAGAACAGGTTGGGTGTGAAGTAAAC 1260
QY 1260 GGGAGTGTAGAGAGGCGTGGTATGGTATGGCGGAGGAGTAGTGTACATAGGGGT 1319
DB 1261 GGGAGTGTAGAGAGGCGTGGGGAATGTATGGCGGAGGAGTAGTGTACATAGGGGT 1320
QY 1320 CATAGTGTAGGCGTGGGCTTTGTTACAAAGTATATCATATAAATAACAGCACTGGAGC 1379
DB 1321 CATAGTGTAGGCGTGGGCTTTGTTACAAAGTATATCATATAAATAACAGCACTGGAGC 1380
QY 1380 CCACCTCCCTGTGACCTGGGTGATCGGGGAGCAGGCGCAGAAATCAACCTTAACTTTTC 1439
DB 1381 CCACCTCCCTGTGACCTGGGTGATCGGGGAGCAGGCGCAGAAATCAACCTTAACTTTTC 1440
QY 1440 TTATTTCTGTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1499
DB 1441 TTATTTCTGTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
QY 1500 AGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1559
DB 1501 AGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
QY 1560 GCTTGACAGTATATCCGAGGTGCGGGAGAGCGGGTGTGAAGATGCCATTTTCTCTTC 1619
DB 1561 GCTTGACAGTATATCCGAGGTGCGGGAGAGCGGGTGTGAAGATGCCATTTTCTCTTC 1620
QY 1620 TCCAGCGGTAAACGGTGGCGGGGTGGAACGAGCGGGGCGGGCGGAGGATCTGGCCAA 1679
DB 1620 TCCAGCGGTAAACGGTGGCGGGGTGGAACGAGCGGGGCGGGCGGAGGATCTGGCCAA 1679

Db	1621	TCCAACGGTACGGTGGCGGGGTGGACAGCCAGGGGGCGGGCGGAGGATCTGGCCAA	1680
Qy	1680	GATGGCTGGCGGGCGGGTGTCTTCTTCTCGGTAACGCCCTCCTTGGATACGTCAATCTG	1739
Db	1681	GATGGCTGGCGGGCGGGTGTCTTCTTCTCGGTAACGCCCTCCTTGGATACGTCAATCTG	1740
Qy	1740	AAAAAGAAAGTGGCGCTGTAATTT	1767
Db	1741	AAAAAGAAAGTGGCGCTGTAATTT	1768
RESULT 3			
AAAF75840			
XX	AAAF75840 standard; DNA; 1768 BP.		
XX	AAAF75840;		
XX	06-AUG-2003 (revised)		
DT	18-MAY-2001 (first entry)		
XX	PCV DNA fragment of Imp 1103 strain.		
DE			
XX	Vaccine; pig; myocarditis; abortion; intrauterine infection;		
KW	multisystemic wasting syndrome; ds.		
XX	Porcine circovirus type 2.		
OS			
XX	WO200116330-A2.		
PN			
XX	08-MAR-2001.		
PD			
XX	28-AUG-2000; 2000WO-EP008781.		
PF			
XX	31-AUG-1999; 99US-0151564P.		
PR			
XX	31-MAY-2000; 2000US-00583350.		
PR			
XX	(MERI-) MERIAL.		
PA	(UYSA-) UNIV SASKATCHEWAN.		
PA	(UYBE-) UNIV QUEENS BELFAST.		
XX	Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Haseard L;		
PI	Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;		
PI	Mcneilly F;		
XX	WPI; 2001-244408/25.		
DR			
XX	Use of porcine circovirus-2 immunogen to formulate a vaccine composition		
PT	to treat pigs against myocarditis, abortion, intrauterine infection		
PT	and/or post-weaning, multisystemic wasting syndrome associated with PCV-		
PT	2.		
XX			
PS	Claim 10; Fig 6 #2; 134pp; English.		
XX			
CC	The present invention relates to the use of porcine circovirus-2 (PCV-2)		
CC	immunogen to formulate a vaccine composition to prevent or treat pigs		
CC	against myocarditis and/or abortion and/or intrauterine infection and/or		
CC	post-weaning, multisystemic wasting syndrome and other pathological		
CC	sequelae associated with PCV-2. The present sequence is a DNA fragment of		
CC	a strain of PCV, which was used in the present invention. (Updated on 06-		
CC	AUG-2003 to correct OS field.)		
XX			
SQ	Sequence 1768 BP; 450 A; 360 C; 496 G; 460 T; 0 U; 2 Other;		
Query Match			
Best Local Similarity 92.6%; Score 1636.8; DB 4; Length 1768;			
Matches 1691; Conservative 2; Mismatches 74; Indels 1; Gaps 1;			
Qy	1	ACCAGGCGCTTCGGCAGCGGCGAGCACCTCGGCAGACCTCAGCAGCAACATGCCCGAGCA	60
Db	1	ACCAGGCGCTTCGGCAGCGGCGAGCACCTCGGCAGACCTCAGCAGCAACATGCCCGAGCA	60
Qy	61	AGAAGATGAAGAAGCGGACCCCAACCCCATAAAGGTGGTGTCTCTGAATAATC	120

Db	61	AGAAGATGAAGAAGCGGACCCCAACCCCATAAAGGTGGTGTCTCTGAATAATC	120
Qy	121	CTTCCGAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCTATTTTGAATATTTTA	180
Db	121	CTTCCGAGACGAGCGCAAGAAATACGGGAGCTCCCAATCTCCTATTTGAATATTTTA	180
Qy	181	TTGTTGGCGAGGAGGTAATGAGGAAGGACGAACCACTCACTCCAGGGTTCGTAATT	240
Db	181	TTGTTGGCGAGGAGGTAATGAGGAAGGACGAACCACTCACTCCAGGGTTCGTAATT	240
Qy	241	TTGTGAAGAACGACAGCTTTTAAATAAGTGAAGTGTATTTGGTGGCCGCTGCCACATCG	300
Db	241	TTGTGAAGAACCAAACTTTTAAATAAGTGAAGTGTATTTGGTGGCCGCTGCCACATCG	300
Qy	301	AGAAAGCGAAAGGACAGATCAGCAGATAAAGAATACTGCAGTAAGAAGCAACTTAC	360
Db	301	AGAAAGCGAAAGGAACTGATCAGCAGATAAAGAATACTGCAGTAAGAAGCAACTTAC	360
Qy	361	TGATGAGTGTGGAGCTCCTAGATCTCAGGGAACAAGGAGTACCTGTCTACTGTGTGA	420
Db	361	TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTACCTGTCTACTGTGTGA	420
Qy	421	GTACCTTGTGGAGAGCGGAGTCTGGTGACCGTTGCAGAGCAGCACCTCTAAAGTTTG	480
Db	421	GTACCTTGTGGAGAGCGGAGTCTGGTGACCGTTGCAGAGCAGCACCTCTAAAGTTTG	480
Qy	481	TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGATGAGCGGGAATAATGCAGAGCGTG	540
Db	481	TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGATGAGCGGGAATAATGCAGAGCGTG	540
Qy	541	ATTGGAAGACTAATGTACACGTCATTGTGGGCGCACCTGGGTGTGGTAAAGCAATGGG	600
Db	541	ATTGGAAGACCAATGTACACGTCATTGTGGGCGCACCTGGGTGTGGTAAAGCAATGGG	600
Qy	601	CTGCTAATTTTCAGACCGCGAAACACATCTCTGGAACACCACTAGAAACAAGTGTGGG	660
Db	601	CTGCTAATTTTCAGACCGCGAAACACATCTCTGGAACACCACTAGAAACAAGTGTGGG	660
Qy	661	ATGCTTACCATGTGAAGAGTGGTTTATTTGATGACTTTTATGCTGGCTGCCCTGGG	720
Db	661	ATGCTTACCATGTGAAGAGTGGTTTATTTGATGACTTTTATGCTGGCTGCCCTGGG	720
Qy	721	ATGATCTACTGAGACTGTGTGATCCATTTGATGACTTTTATGCTGGCTGCCCTGGG	780
Db	721	ATGATCTACTGAGACTGTGTGATCCATTTGATGACTTTTATGCTGGCTGCCCTGGG	780
Qy	781	TACCTTTTGGCGCGCAGTATTCTGATTACCAAGCAATCAGACCCCGTTGGAAATGGTACT	840
Db	781	TACCTTTTGGCGCGCAGTATTCTGATTACCAAGCAATCAGACCCCGTTGGAAATGGTACT	840
Qy	841	CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTCGTATTTT	900
Db	841	CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCTCGTATTTT	900
Qy	901	GGAAAGATGTACAGAAATCCACGAGAGAGGGGCGCAGTTTCGTCAACCTTTCCCGCC	960
Db	901	GGAAAGATGTCTACAGAAATCCACGAGAGAGGGGCGCAGTTTCGTCAACCTTTCCCGCC	960
Qy	961	CATCCCTGAATTTCCCATATGAATAAATTTACTGAGTCTTTTATCACTTCGTAAATGGT	1020
Db	961	CATCCCTGAATTTCCCATATGAATAAATTTACTGAGTCTTTTATCACTTCGTAAATGGT	1020
Qy	1021	TTTTATTATTCA-TTAAAGGTTAAAGTGGGGGCTTTTAAATAATTAATTTCTGAAATTTGA	1079
Db	1021	TTTTATTATTCA-TTAAAGGTTAAAGTGGGGGCTTTTAAATAATTAATTTCTGAAATTTGA	1080
Qy	1080	CATACATGTTTACAGGATATTGTATTTCTGGTTCGTATATCTATCTTTTTCGAACCGAGTGC	1139
Db	1081	CATACAGGTTTACAGGATATTGTATTTCTGGTTCGTATTTACTGTTTTTCGAACCGAGTGC	1140
Qy	1140	CGAGGCTTACGTGGTCTACATTTCCAGCAGTTTCTAGTCTCAGGCAAGCTGTTTCTTT	1199
Db	1141	CGAGGCTTACGTGGTCTCAGATTTCTAGAGTTTCTAGGCTCAGCCTCAGCAAGCTGTTCTTT	1200

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QY 1200 TGTGTTGGTTGGAGTAATCAATAGTGAATCTAGCAGAGTTTGGGGTAAAGTACC 1259
DB 1201 TGTATTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260
QY 1260 GGGAGTGTAGAGAAAGCGCTGGTATTATGTCGGGAGAGTAGTTTACATAGGGGT 1319
DB 1261 GGGAGTGTAGAGAAAGCGTGGGGATTGTATGTCGGGAGAGTAGTTTACATAGGGT 1320
QY 1320 CATAGTCAGGCGCTGCGCTTTGTTACAAAGTTATCATCTAAAGTTATCATCTAAGATTAACAGCAGTGGAGC 1379
DB 1321 CATATGTTGGGCTGTGGCCCTTTGTTACAAAGTTATCATCTAAGATTAACAGCAGTGGAGC 1380
QY 1380 CCACCTCCCTGTACACCTGGGTGATCGGGAGCAGGCGCAGAAATTCACCTTTAACCTTTTC 1439
DB 1381 CCACCTCCCTATCACCTGGGTGATGGGGAGCAGGCGCAGAAATTCACCTTTAACCTTTTC 1440
QY 1440 TTATCTGTAGTAATCAAGGCGCAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAA 1499
DB 1441 TTATCTGTAGTAATCAAGGCGTATAGAGATTTTGTGTCCTCCCTCCCGGGGAACAA 1500
QY 1500 AGTCATTAATTAATGATCTCATGTCACCGCCAGAGGCGTCTGACTGCTGTTTC 1559
DB 1501 AGTCGTCAATTTTAAATCTCATGTCACCGCCAGAGGCGTGTGACTGTGGTAC 1560
QY 1560 GCTTGACAGTATATCCGAAGTGCAGGAGCGGGTGTGAAGATGCCATTTTTCCTTC 1619
DB 1561 GCTTGACAGTATATCCGAAGTGCAGGAGCGGGTGTGAAGATGCCATTTTTCCTTC 1620
QY 1620 TCCAGCGGTAAACGTTGGCGGGGTGGACAGCCAGGGCGCGGAGGATCTGGCCAA 1679
DB 1621 TCCAAACGGTAGCGGTGGCGGGGTGGACAGCCAGGGCGCGGAGGATCTGGCCAA 1680
QY 1680 GATGCTGCGGGCGGTGCTCTCTCTCGGTAAAGCTCTCGATACGTCATATCTG 1739
DB 1681 GATGCTGCGGGCGGTGCTCTCTCTCGGTAAAGCTCTCGATACGTCATATCTG 1740
QY 1740 AAAACGAAGAAGTGCCTGTGAAGTATT 1767
DB 1741 AAAACGAAGAAGTGCCTGTGAAGTATT 1768
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RESULT 4

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ABV72527
ID ABV72527 standard; DNA; 1768 BP.
XX AC ABV72527;
XX
XX 27-OCT-2003 (revised)
XX 29-JAN-2003 (first entry)
XX
DE Nucleotide sequence of porcine circovirus 2 (PCV2).
XX
XX PCV2; mammalian circovirus; virus culture; gene; ss.
XX
XX Porcine circovirus; 2.
XX
XX Key Location/Qualifiers
XX CDS 51..995
XX /*tag= a
XX /note= "ORF1; encodes ABB99414"
XX CDS complement(1034..1735)
XX /*tag= b
XX /note= "ORF2; encodes ABB99415"
XX
XX WO200277210-A2.
XX
XX 03-OCT-2002.
XX
XX 27-MAR-2002; 2002WO-CA000413.
XX
XX 27-MAR-2001; 2001US-0279173P.
XX
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(UWSA-) UNIV SASKATCHEWAN.

Liu Q, Tikoo SK, Willson P, Babiuk LA;

WPI, 2003-029933/02.

P-PSDB; ABB99414, ABB99415.

Culturing a mammalian circovirus in mammalian cells expressing mammalian adenovirus E1 function, useful for molecular biology and biotechnology processes.

Disclosure; Fig 3A; 23pp; English.

The present sequence represents the complete genome of porcine circovirus 2 (PCV2). This sequence comprises two open reading frames (ORFs). PCV2 is cultured using the method of the invention. The specification describes a method for culturing a mammalian circovirus. The method comprises obtaining mammalian cells expressing a mammalian adenovirus E1 function, where the cells are permissive for mammalian circovirus replication; introducing the mammalian circovirus genome, or its portion, into the mammalian cells; and culturing the mammalian cells under conditions suitable for replication of the mammalian circovirus. The method of the invention is useful for culturing circovirus in mammalian cells, expressing mammalian adenovirus E1 function for molecular biology, and biotechnology purposes. (Updated on 27-OCT-2003 to standardise OS field)

Sequence 1768 BP; 463 A; 357 C; 482 G; 466 T; 0 U; 0 Other;

Query Match 91.7%; Score 1620; DB 8; Length 1768;

Best Local Similarity 95.1%; Pred. No. 0;

Matches 1682; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 1 ACCAGCGACATTCGGCAGCGGAGCACCTCGGACAGCCTCAGCAGCAACATGCCAGCA 60

DB 1 ACCAGCGACATTCGGCAGCGGAGCACCTCGGACAGCCTCAGCAGCAACATGCCAGCA 60

QY 61 AGAAGATGGAAGAAAGCGGAGCCCCAACCCCATAAAGTGGGTGTTCACTCTGAATAATC 120

DB 61 AGAAGATGGAAGAAAGCGGAGCCCCAACCCCATAAAGTGGGTGTTCACTCTGAATAATC 120

QY 121 CTTCCGAGAGCGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTTTA 180

DB 121 CTTCCGAGAGCGAGCGCAAGAAATACGGGAGCTCCCAATCTCCCTATTGATATTTTA 180

QY 181 TTGTTGGCAGAGCGGCTTAATGAGGAAGGACGAAACCTCACCTCCAGGGGTTTCGCTAAT 240

DB 181 TTGTTGGCAGAGCGGCTTAATGAGGAAGGACGAAACCTCACCTCCAGGGGTTTCGCTAAT 240

QY 241 TTGTGAAGAGCAGACTTTTAAATAAAGTGAAGTGGTATTGTTGGTGGCCGCTGCCACATCG 300

DB 241 TTGTGAAGAGCAGACTTTTAAATAAAGTGAAGTGGTATTGTTGGTGGCCGCTGCCACATCG 300

QY 301 AGAAGCGGAGGAGCAGATCAGCAGAAATAGAAATACGCAAGTAAAGGCAACTTAC 360

DB 301 AGAAGCGGAGGAGCAGATCAGCAGAAATAGAAATACGCAAGTAAAGGCAACTTAC 360

QY 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGGACAAACGAGTGAACCTGTCTACTGTGTGA 420

DB 361 TTATTTGAATGTGAGCTCCTCGATCTCAAGGACACGAGTGAACCTGTCTACTGTGTGA 420

QY 421 GTACCTTTGTGAGAGCGGAGTCTGGTGAACGTTGTCAGAGCAGCAACCTGTAAAGCTTTG 480

DB 421 GTACCTTTGTGAGAGCGGAGTCTGGTGAACGTTGTCAGAGCAGCAACCTGTAAAGCTTTG 480

QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTCAAAAGTGAAGCGGGAATTCGAGAGCGG 540

DB 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTCAAAAGTGAAGCGGGAATTCGAGAGCGG 540

QY 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACTCGGTGTGTTAAAGCAATGGG 600

DB 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACTCGGTGTGTTAAAGCAATGGG 600

QY 601 CTGCTAATTTTGCAGACCGGAAACCATACATCTGGAAACCACTAGAAAACAAGTGTGGG 660

Db	1681	GATGGCTGGGGGGGGTGTCTTCTTTCGCGTAACGCTCTCTTGGATACGTATAGCTG	1740
Qy	1740	AAAAACGAAGAAGTCGCTGTAAGTATT	1767
Db	1741	AAAAACGAAGAAGTCGCTGTAAGTATT	1768
RESULT 5			
AX83755	AX83755 standard; DNA; 1786 BP.		
ID	AX83755		
XX	AX83755;		
AC	XX		
XX	27-AUG-1999 (first entry)		
DT	XX		
XX	Porcine circovirus type II 9741 nucleotide sequence.		
DE	XX		
XX	Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;		
KW	postweaning multisystemic wasting syndrome virus; diagnosis; ds.		
KW	Porcine circovirus.		
OS	XX		
XX	WO9929717-A2.		
PN	XX		
XX	17-JUN-1999.		
PD	XX		
XX	11-DEC-1998; 98WO-CA001130.		
PF	XX		
XX	11-DEC-1997; 97US-0069233P.		
PR	16-DEC-1997; 97US-0069750P.		
XX	(UYSA-) UNIV SASKATCHEWAN.		
PA	XX		
XX	Wang L, Babiuk LA, Potter AA, Willson P;		
PI	XX		
XX	WPI; 1999-394957/33.		
DR	XX		
XX	New isolated porcine circovirus Type II.		
PT	XX		
XX	Claim 1; Fig 4; 82pp; English.		
PS	XX		
XX	The present invention describes a new isolated porcine circovirus Type II		
CC	(PCVII), obtained from postweaning multisystemic wasting syndrome-		
CC	affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide sequences.		
CC	AAV24929 to AAV24934 represent PCVII open reading frame (ORF) proteins		
CC	(N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not correspond exactly		
CC	with the PCVII ORFs given in Fig 3A to Fig 3D). The PCVII polypeptides		
CC	can be used for treating or preventing PCVII infection in vertebrates.		
CC	The products can also be used to detect the PCVII		
XX	Sequence 1786 BP; 467 A; 367 C; 481 G; 471 T; 0 U; 0 Other;		
SQ			
Query Match 87.5%; Score 1545.4; DB 2; Length 1786;			
Best Local Similarity 94.3%; Pred. No. 0;			
Matches 1673; Conservative 0; Mismatches 86; Indels 16; Gaps 6;			
Qy	1	ACCAGCGACCTTGGCAGCGGCGACCTCGGAGCAGCCTCAGCAGCAATGCCAGCA	60
Db	1	ACCAGCGACCTTGGCAGCGGCGACCTCGGAGCAGCCTCAGCAGCAATGCCAGCA	60
Qy	61	AGAGAAATGGAAGAGCGGACCCCAACCCCAATAAAGGTGGTGTTCACCTCTGAAATAATC	120
Db	61	AGAGAAATGGAAGAGCGGACCCCAACCCCAATAAAGGTGGTGTTCACCTCTGAAATAATC	120
Qy	121	CTTCCGAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA	180
Db	121	CTTCCGAGACGAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTTTAA	180
Qy	181	TTGTTGGCAGAGGGTTAATGAGGAAGCAACACCTCACCTCCAGGGGTTCGCTAATT	240
Db	181	TTGTTGGCAGAGGGTTAATGAGGAAGCAACACCTCACCTCCAGGGGTTCGCTAATT	240
Qy	241	TTGTGAAGAAGCAGACACTTTTAAATGAAGTGGTATTTGGGTGCCCGCTGCCACATCG	300


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Db 241 TTTGGAAGCAAACTTTAATAAGTGAAGTGGTATTTGGTGGCCGCTGCCACATCG 300
Qy 301 AGAAGCCAAAGGACACATCAGCAGATAAGATATCTGCAGTAAAGAGCAACTTAC 360
Db 301 AGAAGCCAAAGGAACTGATCAGCAAAATAAAGAAATATTGCAGTAAAGAGCAACTTAC 360
Qy 361 TGATGGAGTGGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGTGTGA 420
Db 361 TTAATGATGTGGAGCTCTCGATCTCAAGGACAGCAGCGACCTGTCTACTGTGTGA 420
Qy 421 GTAACCTTGTGGAGAGCGGAGTGTGGTGAACGTTTGCAGAGCAGCACCTGTAAAGCTTTG 480
Db 421 GTACCTTGTGGAGAGCGGAGTGTGGTGAACGTTTGCAGAGCAGCACCTGTAAAGCTTTG 480
Qy 481 TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGAAGGAGGGAATGCAAGAGCGTG 540
Db 481 TCAAAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGAAGGAGGGAATGCAAAAAGCGTG 540
Qy 541 ATTGAAGACTAATGTACACGCTCATTTGTGGGCGCACCTGGGTGTGGTAAAGCAAAATGGG 600
Db 541 ATTGAAGAAACCAATGTACACTTGTGGGCGCACCTGGGTGTGGTAAAGCAAAATGGG 600
Qy 601 CTGCTAAATTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 660
Db 601 CTGCTAAATTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 660
Qy 661 ATGGTTACATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Db 661 ATGGTTACATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCGACTGTAGAGACTAAAGGTGGAACCTG 780
Db 721 ATGATCTACTGAACTGTGTGATCGATATCCATTCGACTGTAGAGACTAAAGGTGGAACCTG 780
Qy 781 TACCTTTTGTGGCCGCGAGTATCTGATACAGCAATCAGACCCCGTTGGGAATGGTACT 840
Db 781 TACCTTTTGTGGCCGCGAGTATCTGATACAGCAATCAGACCCCGTTGGGAATGGTACT 840
Qy 841 CTTCAACTGCTGCCAGCTGTAGAAGCTCTCTATCGGAGGATTAATCTCTTGGTATTTT 900
Db 841 CTTCAACTGCTGCCAGCTGTAGAAGCTCTCTATCGGAGGATTAATCTCTTGGTATTTT 900
Qy 901 GGAAGATGCTACAGAAACCAATCCAGAGGAAACCCGGGGCGAGTTGTACCCCTTCC 957
Db 901 GGAAGATGCTACAGAAACCAATCCAGAGGAAACCCGGGGCGAGTTGTACCCCTTCC 957
Qy 958 CCCCATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTT---TTATCACTCGT 1014
Db 961 CCCCATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTT---TTATCACTCGT 1020
Qy 1015 AATGGTTTTATTTATTAATAAGG---TTAAGTGGGGGCTTTAAATTAATTTCTCTGA 1073
Db 1021 AATGGTTTTATTTATTTATTTAGGGTTTAAAGTGGGGGCTTTAAAGATTAATTTCTCTGA 1080
Qy 1074 ATTGTACATACATGTTTACACGATATGATTTCTCTGGTC---GTATATAGTGTTCGAAAC 1132
Db 1081 ATTGTACATACATGTTTACACGATATGATTTCTCTGGTC---GTATATAGTGTTCGAAAC 1140
Qy 1133 GCAGTCCGAGGCTACGTGGTCTCATTTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGG 1192
Db 1141 GCAGTCCGAGGCTACGTGGTCTCATTTTCCAGAGTTTGTAGCTCAGCCACAGCAAGCTGA 1200
Qy 1193 TTTCTTTTGTGTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTA 1252
Db 1201 TTTCTTTTGTGTGGTGGAGTAAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTG 1260
Qy 1253 AAGTACCGGAGCTGTAGGAGGCTGGTTTATGCTATGGCGGAGGAGTAGTTTACA 1312
Db 1261 AAGTACCGGAGCTGTAGGAGGCTGGTTTATGCTATGGCGGAGGAGTAGTTTACA 1320
Qy 1313 TAGGGGTCTAGTGTAGGCTGTGGCTTTGTTTACAAAGTATCATCTTAAATAACAGCA 1372
Db 1313 TAGGGGTCTAGTGTAGGCTGTGGCTTTGTTTACAAAGTATCATCTTAAATAACAGCA 1372
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Db 1321 TATGGTCAATAGTGTAGGCTGTGGCTTTGTTTACAAGTTATCATCTAAATAACAGCA 1380
Qy 1373 CTGAGGCCACTCCCTGTGTACCCCTGGGTGATCGGGAGCAGGGCCAGAAATTCACCTTA 1432
Db 1381 GTGGAGCCACTCCCTGTGTATCACCCCTGGGTGATGGGAGCAGGGCCAGAAATTCACCTTA 1440
Qy 1433 ACCTTTCTTATCTGTAGTATTTCAAGGCAACAGAGGGGGTGTGACCCCTCTCTGGG 1492
Db 1441 ACCTTTCTTATCTGTAGTATTTCAAGGCAATAGAGATTTTGTGGTCCCCCTCCCGG 1500
Qy 1493 GGAAGAGTCATTAATTAATTCATCTCATGTCTCCACCCGAGGAGGGGTCTCTGACT 1552
Db 1501 GGAACAAAGTCGTCAATTTTAAATCTCATGTCTCCACCCGAGGAGGGGTCTCTGACT 1560
Qy 1553 GTGGTTCCTTTGACAGTATATCCGAAGGTGGGAGAGCGGGTGTGGAAGATGCCATTT 1612
Db 1561 GTGGTACGTTGACAGTATATCCGAAGGTGGGAGAGCGGGTGTGGAAGATGCCATTT 1620
Qy 1613 TTCTTTCTCCAGCGGTAAACGGT-----GGCGGGGTGAGACGACCCAGGGCGGGCGG 1665
Db 1621 TTCTTTCTCCAAACGCTAGCGGTTTCTGAAGCGGGGGTGGACGACCCAGGGCGGGCGG 1680
Qy 1666 GAGGATCTGGCCAAAGATGGCTGCGGGGGCGGTGTCTTCTCTCGGTAAACGCTCTCTGG 1725
Db 1681 GAGGATCTGGCCAAAGATGGCTGCGGGGGCGGTGTCTTCTCTCGGTAAACGCTCTCTGG 1740
Qy 1726 ATAGCTCATATCTGAAAAC-GAAAAGAGTGCGCTG 1759
Db 1741 ATAGCTCATAGCTGAAAACCTGAAAGATGCGCTG 1775
```

RESULT 6

AAK35378

ID AAK35378 standard; DNA; 1767 BP.

XX AAK35378;

XX 07-JUL-1999 (first entry)

XX Nucleotide sequence of PCV isolate Imp1011-48121.

XX PCV isolate; type II porcine circovirus; PCV; PMWS;
XX porcine multisystemic wasting syndrome; pig; vaccine; ss.

XX Porcine circovirus.

XX WO918214-A1.

XX 15-APR-1999.

XX 01-OCT-1998; 98WO-FR002107.

XX 03-OCT-1997; 97FR-00012382.

XX 22-JAN-1998; 98FR-00000873.

XX 20-MAR-1998; 98FR-00003707.

XX (MERI-) MERIAL.

XX (UYBE-) UNIV QUEBENS BELFAST.

XX (UYSA-) UNIV SASKATCHEWAN.

XX Allan G, Meehan B, Clark E, Ellis J, Haines D, Hassard L;
XX Harding J, Charreyre CE, Chappuis GE;

XX WPI; 1999-264024/22.

XX New type II porcine circovirus.

XX Claim 11; Fig 1; 56pp; French.

XX The present sequence represents the nucleotide sequence of PCV isolate
XX Imp1011-48121. The specification describes a preparation of type II
XX porcine circovirus (PCV), which is particularly isolated from a lesion,
XX from a pig with symptoms of PMWS (porcine multisystemic wasting

CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,
CC and vectors that express these polypeptides are all useful in vaccines,
CC suitable for administration to adult or young pigs, or to pregnant sows
CC (for passive immunization of their offspring). DNA isolated from PCV is
CC used for in vivo or in vitro expression of viral polypeptides, also as
CC probes or primers for diagnosis in usual hybridization or amplification
CC assays. These polypeptides may also be used diagnostically to detect PCV-
CC specific antibodies, while antibodies raised against the polypeptides can
CC be used to detect antigens, in any usual immunoassay format
XX
SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;
Query Match 79.9%; Score 1412; DB 2; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACCAGCGACCTTCGGCAGCGCAGCAGCCTCCGCGAGCAGCCTCAGCAGCAATGCCAGCA 60
DB 348 ACCAGCGACCTTCGGCAGCGCAGCAGCCTCCGCGAGCAGCCTCAGCAGCAATGCCAGCA 407
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTCTCACTCTGAATAATC 120
DB 408 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTCTCACTCTGAATAATC 467
QY 121 CTTCCGAAGACGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTATTTTA 180
DB 468 CTTCCGAAGACGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTATTTTA 527
QY 181 TTGTGGCGAGGAGGATTAATGAGGAAGCAGCAACCTCACCTCCAGGGGTTCCTAATT 240
DB 528 TTGTGGCGAGGAGGATTAATGAGGAAGCAGCAACCTCACCTCCAGGGGTTCCTAATT 587
QY 241 TTGTGAAAGACAGACTTTTAATAAGTGAAGTGTATTTGGGTCCCGCTGCCACATCG 300
DB 588 TTGTGAAAGACAGACTTTTAATAAGTGAAGTGTATTTGGGTCCCGCTGCCACATCG 647
QY 301 AGAAGCGAAGGACAGATCAGCAGAAATGAAGATCTGCAGTAAAGAGCGCAACTTAC 360
DB 648 AGAAGCGAAGGACAGATCAGCAGAAATGAAGATCTGCAGTAAAGAGCGCAACTTAC 707
QY 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGAGTGACCTGTCTACTGTGTA 420
DB 708 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGAGTGACCTGTCTACTGTGTA 767
QY 421 GTACCTTTGTGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTG 480
DB 768 GTACCTTTGTGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTG 827
QY 481 TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCAGAACGCTG 540
DB 828 TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCAGAACGCTG 887
QY 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGCGCACCTGGGTGTGTTAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACAGCTCATTTGTGGGCGCACCTGGGTGTGTTAAAGCAATGGG 947
QY 601 CTGCTAATTTTCAGACCCGGAACCAACATCTGGAACCCACCTAGAAACAGTGTGGG 660
DB 948 CTGCTAATTTTCAGACCCGGAACCCACATCTGGAACCCACCTAGAAACAGTGTGGG 1007
QY 661 ATGGTTACCATGGTGAAGAGTGTGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 1008 ATGGTTACCATGGTGAAGAGTGTGTTGTTATGATGACTTTTATGGCTGGCTGCCCTGGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATTCGATATCCATTGACTGTAGAGCTAAGGTGGAACCTG 780
DB 1068 ATGATCTACTGAGACTGTGTGATTCGATATCCATTGACTGTAGAGCTAAGGTGGAACCTG 1127
QY 781 TACCTTTTGGCCCGCAGTATCTGATTTACAGCAATCAGACCCCGTTGGATGTGACT 840
DB 1128 TACCTTTTGGCCCGCAGTATCTGATTTACAGCAATCAGACCCCGTTGGATGTGACT 1187
QY 841 CCTCAACTGTCTCCCGAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTCTGGTATTTT 900

DB 1188 CCTCAACTGTCTCCCGAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTCTGGTATTTT 1247
QY 901 GGAAGATGCTACAGAAACAATCCACGAGGAGGAGGCGCAGTTCTGTCAACCTTTTCCCCC 960
DB 1248 GGAAGATGCTACAGAAACAATCCACGAGGAGGAGGCGCAGTTCTGTCAACCTTTTCCCCC 1307
QY 961 CATGCCCTGAATTTCCATATGAATTAATTAAGTCTTCTTTTATCACTTCGTGAATGGT 1020
DB 1308 CATGCCCTGAATTTCCATATGAATTAATTAAGTCTTCTTTTATCACTTCGTGAATGGT 1367
QY 1021 TTTTATTTATTAAGGTTAAGTGGGGCTTTAAATTAATAATTTCTCTGAATTTGATAC 1080
DB 1368 TTTTATTTATTAAGGTTAAGTGGGGCTTTAAAGATTAATAATTTCTCTGAATTTGATAC 1427
QY 1081 ATACATGGTTTACACGATATTTCTTCTGGTCTGATATATCTGTTTTCGAAACGAGTGCC 1140
DB 1428 ATACATGGTTTACACGATATTTCTTCTGGTCTGATATATCTGTTTTCGAAACGAGTGCC 1487
QY 1141 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
DB 1488 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1547
QY 1201 GTTGTGGTTGGAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGGTAAAGTAGCG 1260
DB 1548 GTTGTGGTTGGAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGGTAAAGTAGCG 1607
QY 1261 GAGTGTAGGAGAGGCGCTGGCTTATGATGCGCGGAGGAGTAGTATTTACATAGGGGTC 1320
DB 1608 GAGTGTAGGAGAGGCGCTGGCTTATGATGCGCGGAGGAGTAGTATTTACATAGGGGTC 1667
QY 1321 ATAGTGTAGGGCTGTGGCTTTGTTTACAAGTTATCATCTAAATTAACAGCTGAGCC 1380
DB 1668 ATAGTGTAGGGCTGTGGCTTTGTTTACAAGTTATCATCTAGAATAACAGCTGAGCC 1727
QY 1381 CACTCCCTGTCAACCTGGTGATCGGGAGCAGGCGCAG 1420
DB 1728 CACTCCCTGTCAACCTGGTGATCGGGAGCAGGCGCAG 1767
RESULT 7
AAK35210
ID AAK35210 standard; DNA; 1767 BP.
XX
XX AAK35210;
AC AC
XX AC
DT 01-JUL-1999 (first entry)
XX
DE Nucleotide sequence of PCV isolate Impl011-48121.
XX
KW PCV isolate; type II porcine circovirus; PCV; PMWS;
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX Porcine circovirus.
OS
XX FR2769322-A1.
FN
XX 09-APR-1999.
PD
XX 22-JAN-1998; 98FR-00000873.
PF
XX 03-OCT-1997; 97FR-00012382.
PR
XX (MERI-) MERIAL SAS.
PA
XX Allan G, Meahan B, Clark E, Ellis J, Haines D, Haseard L;
PI Harding J, Charreyre CE, Chappuis GE;
XX WPI; 1999-246948/21.
DR New type II porcine circovirus, used for, e.g. passive immunization of
XX pregnant sows.
PT
XX

PS Claim 14; Fig 1; 48pp; French.

XX The present sequence represents the nucleotide sequence of PCV isolate
 CC Impl011-48121. The specification describes a preparation of type II
 CC porcine circovirus (PCV), which is particularly isolated from a lesion,
 CC from a pig with symptoms of PMWS (porcine multisystemic wasting
 CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,
 CC and vectors that express these polypeptides are all useful in vaccines,
 CC suitable for administration to adult or young pigs, or to pregnant sows
 CC (for passive immunization of their offspring). DNA isolated from PCV is
 CC used for in vivo or in vitro expression of viral polypeptides, also as
 CC probes or primers for diagnosis in usual hybridization or amplification
 CC assays. These polypeptides may also be used diagnostically to detect PCV-
 CC specific antibodies, while antibodies raised against the polypeptides can
 CC be used to detect antigens, in any usual immunoassay format

XX SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;

Query Match 79.9%; Score 1412; DB 2; Length 1767;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	ACCAGCGCATTCCGCGAGCGGAGCAGCCTCGCAGCAGCCTCAGCAGCAACATGCCAGCA	60
DB	348	ACCAGCGCATTCCGCGAGCGGAGCAGCCTCGCAGCAGCCTCAGCAGCAACATGCCAGCA	407
QY	61	AGAAAGATGGAAAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC	120
DB	408	AGAAAGATGGAAAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC	467
QY	121	CTTCCGAGACGAGCGGCAAGAAATACGGGATCTTCCAAATATCCCTATTGATATTTTA	180
DB	468	CTTCCGAGACGAGCGGCAAGAAATACGGGATCTTCCAAATATCCCTATTGATATTTTA	527
QY	181	TTGTGGCGAGGAGGTATAGAGAGAGCAACCTCACTCAGGGGTTTCGCTAAT	240
DB	528	TTGTGGCGAGGAGGTATAGAGAGAGCAACCTCACTCAGGGGTTTCGCTAAT	587
QY	241	TTGTGAGAGCAGACTTTTATTAAGTGAAGTGTATTTGGTTCGCGCTCCACATCG	300
DB	588	TTGTGAGAGCAGACTTTTATTAAGTGAAGTGTATTTGGTTCGCGCTCCACATCG	647
QY	301	AGAAAGCGAAAGCAAGATCAGCAGATAAAGATATCTGCAGTAAAGAGGCAACTTAC	360
DB	648	AGAAAGCGAAAGCAAGATCAGCAGATAAAGATATCTGCAGTAAAGAGGCAACTTAC	707
QY	361	TGATGAGTGTGGAGCTCTAGATCTCAGGCAACCGAGTGACCTGTCTACTGTGTGA	420
DB	708	TGATGAGTGTGGAGCTCTAGATCTCAGGCAACCGAGTGACCTGTCTACTGTGTGA	767
QY	421	GTACCTTTTGGAGCGGAGTCTGTGACCGTTTCAGAGCAGCAGCCTGTAAAGCTTTG	480
DB	768	GTACCTTTTGGAGCGGAGTCTGTGACCGTTTCAGAGCAGCAGCCTGTAAAGCTTTG	827
QY	481	TCAAGAAATTTCCGCGGGTGGCTGAACTTTTGAAGTGAGCGGAAATTCAGAACGCTG	540
DB	828	TCAAGAAATTTCCGCGGGTGGCTGAACTTTTGAAGTGAGCGGAAATTCAGAACGCTG	887
QY	541	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACTGGGTGTGTAAAGCAATGGG	600
DB	888	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACTGGGTGTGTAAAGCAATGGG	947
QY	601	CTGCTAATTTTGAGACCGGAAACCACTACTGGAACCACTAGAAACAGTGGTGGG	660
DB	948	CTGCTAATTTTGAGACCGGAAACCACTACTGGAACCACTAGAAACAGTGGTGGG	1007
QY	661	ATGGTTACCATGTGAAGAGTGGTTGTTATTCATGACTTTTATGCTGCTGCCCTGGG	720
DB	1008	ATGGTTACCATGTGAAGAGTGGTTGTTATTCATGACTTTTATGCTGCTGCCCTGGG	1067
QY	721	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAC	780
DB	1068	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAC	1127

QY	781	TACCTTTTGGCCCGCAGTATTCTGATTACCAACAATCAGACCCCGTTGGAATGGTACT	840
DB	1128	TACCTTTTGGCCCGCAGTATTCTGATTACCAACAATCAGACCCCGTTGGAATGGTACT	1187
QY	841	CCTCAACTGCTGTCCTCCAGCTGTAGAAGCTCTTTATCGAGGATTACTTCTTGGTATTTT	900
DB	1188	CCTCAACTGCTGTCCTCCAGCTGTAGAAGCTCTTTATCGAGGATTACTTCTTGGTATTTT	1247
QY	901	GGAAAGATGCTTACAGAAACAATCCACGGAGGAGGGGCCAGTTCGTCACTTCCCTCC	960
DB	1248	GGAAAGATGCTTACAGAAACAATCCACGGAGGAGGGGCCAGTTCGTCACTTCCCTCC	1307
QY	961	CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTA	1020
DB	1308	CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTA	1367
QY	1021	TTTTTATTTATTCATTAAGGGTTAAGTGGGGGCTCTTTAAATTTAAATTTCTCTGAAT	1080
DB	1368	TTTTTATTTATTCATTAAGGGTTAAGTGGGGGCTCTTTAAAGATTAAATTTCTCTGAAT	1427
QY	1081	ATACATGTTTACACGGGATTTGTTATTCCTGCTCGTATATCTGTTTTCGAAACGCA	1140
DB	1428	ATACATGTTTACACGGGATTTGTTATTCCTGCTCGTATATCTGTTTTCGAAACGCA	1487
QY	1141	GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT	1200
DB	1488	GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT	1547
QY	1201	GTGTTGGTTGGTGAAGTAATCAATAGTCAATCTAGGACAGGTTTGGGGGTAAAGTAC	1260
DB	1548	GTGTTGGTTGGTGAAGTAATCAATAGTCAATCTAGGACAGGTTTGGGGGTAAAGTAC	1607
QY	1261	GGAGTGTAGCAGAGGAGGCTGGGTTATGTTATGCGGAGGAGGAGTATTTACATAGG	1320
DB	1608	GGAGTGTAGCAGAGGAGGCTGGGTTATGTTATGCGGAGGAGGAGTATTTACATAGG	1667
QY	1321	ATAGTGAGGCTGTGGCTTTGTTTACAAAGTTTATCATCTAAATTAACAGCACTGGAG	1380
DB	1668	ATAGTGAGGCTGTGGCTTTGTTTACAAAGTTTATCATCTAAATTAACAGCACTGGAG	1727
QY	1381	CATCCCTCTGTCAACCTGGGTGATCGGGGAGCAGGGCCAG	1420
DB	1728	CATCCCTCTGTCAACCTGGGTGATCGGGGAGCAGGGCCAG	1767

RESULT 8

AZ56869
 ID AA256869 standard; DNA; 1767 BP.

XX AC AZ56869;

XX DT 25-APR-2000 (first entry)

XX DE DNA sequence of PCV Imp.1011-48121 isolate.

XX KW Antigen; porcine multisystemic wasting syndrome; PMWS; antiviral;

XX KW porcine circovirus; PCV; porcine parvovirus; PPV; vaccination; ds.

XX OS Porcine circovirus.

XX PN WO200001409-A2.

XX PD 13-JAN-2000.

XX PF 28-JUN-1999; 99WO-EP004698.

XX PR 06-JUL-1998; 98PR-00008777.

XX PA (MERI-) MERIAL.

XX PA (UYBE-) UNIV QUEENS BELFAST.

XX PA (UYSA-) UNIV SASKATCHEWAN.

XX XX

PI Allan GM, Meehan BM, Ellis JA, Krakowka GS, Audonnet JF;
XX WPI; 2000-182091/16.
XX Use of a porcine circovirus antigen and a porcine parvovirus antigen for
XX vaccination against porcine multisystemic wasting syndrome.
XX Disclosure; Fig 1; 6lpp; English.
XX The invention provides a novel antigenic preparation directed against
XX porcine multisystemic wasting syndrome (PMWS) that comprises porcine
XX circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV
XX antigens and PPV antigens can be used for vaccination against PMWS. The
XX present sequence represents the DNA sequence of PCV Imp.1011-48121
XX isolate
SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;
Query Match 79.9%; Score 1412; DB 3; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACCAGCGACATTGGCAGCGGAGCAGCCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGCGACATTGGCAGCGGAGCAGCCTCGCAGCACCTCAGCAGCAACATGCCAGCA 407
QY 61 AGAAGATGGAAGACGGGACCCCAACCCCAATAAAGGTGGTTCACCTCGAATATC 120
DB 408 AGAAGATGGAAGACGGGACCCCAACCCCAATAAAGGTGGTTCACCTCGAATATC 467
QY 121 CTTCCGAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTT 180
DB 468 CTTCCGAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTT 527
QY 181 TTGTTGGCAGGAGGTTAATGAGGAGGACGAAACACCTCACCTCAGGGGTCGCTAAT 240
DB 528 TTGTTGGCAGGAGGTTAATGAGGAGGACGAAACACCTCACCTCAGGGGTCGCTAAT 587
QY 241 TTGTTGAGGAGGAGCTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
DB 588 TTGTTGAGGAGGAGCTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 647
QY 301 AGAAGCGAAGGAGGAGCTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 360
DB 648 AGAAGCGAAGGAGGAGCTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 707
QY 361 TGATGAGTGTGGAGCTCCTAGATCTCAGGGAACAAGGAGTCACTGTCTACTGTGTA 420
DB 708 TGATGAGTGTGGAGCTCCTAGATCTCAGGGAACAAGGAGTCACTGTCTACTGTGTA 767
QY 421 GTACCTTTGGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG 480
DB 768 GTACCTTTGGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG 827
QY 481 TCAGAAATTTCCGCGGGCTGGCTGAATTTTGAAGTGAAGGAGGAGGAGGAGGAGGAG 540
DB 828 TCAGAAATTTCCGCGGGCTGGCTGAATTTTGAAGTGAAGGAGGAGGAGGAGGAGGAG 887
QY 541 ATTGGAAGACTAATATACAGTCACTTTGTTGGGGCCACCTGGGTGTGTAAAGCAATGG 600
DB 888 ATTGGAAGACTAATATACAGTCACTTTGTTGGGGCCACCTGGGTGTGTAAAGCAATGG 947
QY 601 CTGCTAATTTTTCAGACCCGGAACACATCTCTGGAACACCTAGAAACAGTGTGGG 660
DB 948 CTGCTAATTTTTCAGACCCGGAACACATCTCTGGAACACCTAGAAACAGTGTGGG 1007
QY 661 ATGGTTACCATGTGGAAGAGTGGTGTATTTGATGATCTTTATGGCTGGCTGCCCTGG 720
DB 1008 ATGGTTACCATGTGGAAGAGTGGTGTATTTGATGATCTTTATGGCTGGCTGCCCTGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGATCTAGACATTAAGTGGACTG 780
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTGATCTAGACATTAAGTGGACTG 1127

QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTACCGCAATCAGACCCCGTTGGAATGGTACT 840
DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTACCGCAATCAGACCCCGTTGGAATGGTACT 1187
QY 841 CTTCAACTGCTGTCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTTCCCTGGTATTTT 900
DB 1188 CTTCAACTGCTGTCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTTCCCTGGTATTTT 1247
QY 901 GGAAGATGCTACAGAACAAATCCAGGAGGAGGGGCGAGTTCGTCAACCTTTCCCTCCC 960
DB 1248 GGAAGATGCTACAGAACAAATCCAGGAGGAGGGGCGAGTTCGTCAACCTTTCCCTCCC 1307
QY 961 CATGCCCTGAAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 1308 CATGCCCTGAAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1367
QY 1021 TTTTATTTATTAAGGTTAAGTGGGGGCTTTAAATTAATTAATTAATTAATTAATTAAT 1080
DB 1368 TTTTATTTATTAAGGTTAAGTGGGGGCTTTAAATTAATTAATTAATTAATTAATTAAT 1427
QY 1081 ATACATGTTTACACGATATTTCTGCTGCTGCTATATCTGCTGCTGCTGCTGCTGCT 1140
DB 1428 ATACATGTTTACACGATATTTCTGCTGCTGCTATATCTGCTGCTGCTGCTGCTGCT 1487
QY 1141 GAGGCTCTAGTGTCTTACATTTCCAGCATTTTGTAGTCTCAGCCACAGCTGTTCTTTT 1200
DB 1488 GAGGCTCTAGTGTCTTACATTTCCAGCATTTTGTAGTCTCAGCCACAGCTGTTCTTTT 1547
QY 1201 GTTGTGTTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1260
DB 1548 GTTGTGTTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1607
QY 1261 GAGTGTGAGGAGGAGGCTGAGTATGATGATGCGGAGGAGGAGTATTTACATAGGGGTC 1320
DB 1608 GAGTGTGAGGAGGAGGCTGAGTATGATGATGCGGAGGAGGAGTATTTACATAGGGGTC 1667
QY 1321 ATAGGTGAGGCTGTGGCTTTGTTTCAAGTATCATCTAAATTAACAGCACTGGAGCC 1380
DB 1668 ATAGGTGAGGCTGTGGCTTTGTTTCAAGTATCATCTAAATTAACAGCACTGGAGCC 1727
QY 1381 CACTCCCTGTCAACCTGGGTGATCGGGAGCAGGCGCAG 1420
DB 1728 CACTCCCTGTCAACCTGGGTGATCGGGAGCAGGCGCAG 1767

RESULT 9
AAF75835
ID AAF75835 standard; DNA; 1767 BP.
XX
AC AAF75835;
XX
XX
DT 06-AUG-2003 (revised)
DT 18-MAY-2001 (first entry)
XX
XX PCV DNA fragment of Imp 1011-48121 strain.
DE
XX Vaccine; pig; myocarditis; abortion; intrauterine infection;
KW multisystemic wasting syndrome; ds.
XX
XX Porcine circovirus type 2.
XX
XX WO200116330-A2.
XX
XX 08-MAR-2001.
XX
XX 28-AUG-2000; 2000WO-EP008781.
XX
XX 31-AUG-1999; 99US-0151564P.
PR 31-MAY-2000; 2000US-00583350.
XX
XX (MERI-) MERIAL.
PA (UISA-) UNIV SASKATCHEWAN.
PA

PA (UYBE-) UNIV QUEENS BELFAST.
XX Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;
PI Mcneilly F;
XX WPI; 2001-244408/25.
DR
XX
XX Use of porcine circovirus-2 immunogen to formulate a vaccine composition
PT to treat pigs against myocarditis, abortion, intrauterine infection
PT and/or post-weaning, multisystemic wasting syndrome associated with PCV-
PT 2.
XX
XX Disclosure; Fig 1 #2; 134pp; English.
XX
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)
CC immunogen to formulate a vaccine composition to prevent or treat pigs
CC against myocarditis and/or abortion and/or intrauterine infection and/or
CC post-weaning, multisystemic wasting syndrome and other pathological
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of
CC a strain of PCV, which was used in the present invention. (Updated on 06-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;
Query Match 79.9%; Score 1412; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACCAGCGCACTTCGGCAGCGGAGCACTTCGCGACACCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGGCAGCGGAGCACTTCGCGACACCTCAGCAGCAACATGCCAGCA 407
QY 61 AGAAGATGGAAGACGACGCCACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC 120
DB 408 AGAAGATGGAAGACGACGCCACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC 467
QY 121 CTTCCGACGACGCGCAAGAAATAACGGGATCTTCCAAATATCCCTATTGATATTTTA 180
DB 468 CTTCCGACGACGCGCAAGAAATAACGGGATCTTCCAAATATCCCTATTGATATTTTA 527
QY 181 TTGTGGCAGGAGGTAATAGGAGAGGACGAACACCTCACCCTCAGCGGTTTCGTAAT 240
DB 528 TTGTGGCAGGAGGTAATAGGAGAGGACGAACACCTCACCCTCAGCGGTTTCGTAAT 587
QY 241 TTGTGAAGACGACATTTTAATAAGTGAAGTGAATTTGGTGGCCGCTGCCACATCG 300
DB 588 TTGTGAAGACGACATTTTAATAAGTGAAGTGAATTTGGTGGCCGCTGCCACATCG 647
QY 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATACCTGAGTAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATACCTGAGTAAGAGGCAACTTAC 707
QY 361 TGATGGAGTGTGGAGTCTCCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGTGTA 420
DB 708 TGATGGAGTGTGGAGTCTCCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGTGTA 767
QY 421 GTACCTTTTGGAGAGCGGGAGTCTGTGACCGTTCAGAGCAGCAACCTGTAAACGTTTG 480
DB 768 GTACCTTTTGGAGAGCGGGAGTCTGTGACCGTTCAGAGCAGCAACCTGTAAACGTTTG 827
QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAGCGGAAATTCAGAACCGTG 540
DB 828 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAGCGGAAATTCAGAACCGTG 887
QY 541 ATTGGAAGACTAATGTACAGTCACTATTGTGGGGCCACTGTGGTGTGTAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACAGTCACTATTGTGGGGCCACTGTGGTGTGTAAGCAATGGG 947
QY 601 CTGCTAATTTTGCAGACCGGAAACCACTATCTGGAACCACTAGAAAACAGTGTGGG 660
DB 948 CTGCTAATTTTGCAGACCGGAAACCACTATCTGGAACCACTAGAAAACAGTGTGGG 1007

QY 661 ATGTTACCATGTGAAGAAAGTGGTTTATTTATGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 1008 ATGTTACCATGTGAAGAAAGTGGTTTATTTATGATGACTTTTATGGCTGGCTGCCCTGGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAACCTG 780
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAACCTG 1127
QY 781 TACCTTTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
DB 1128 TACCTTTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 1187
QY 841 CCTCAACTGTCTGCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTCTGGTATTTT 900
DB 1188 CCTCAACTGTCTGCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTCTGGTATTTT 1247
QY 901 GGAAGATGCTACAGAACAAATCCAGGAGGAGGGGCGAGTTCGTCAACCTTTTCCCGCC 960
DB 1248 GGAAGATGCTACAGAACAAATCCAGGAGGAGGGGCGAGTTCGTCAACCTTTTCCCGCC 1307
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAAGTCTTTTATCACTCTCGTAAATGGT 1020
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAAGTCTTTTATCACTCTCGTAAATGGT 1367
QY 1021 TTTTATTAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTTCTCTGAATTTGAC 1080
DB 1368 TTTTATTAATTAAGGTTAAGTGGGGGTCTTTAAAGTAAATTTCTCTGAATTTGAC 1427
QY 1081 ATACATGTTTACAGGATATTTGATTTCTGTTGCTGATATCTGTTTTCGACGAGTGCC 1140
DB 1428 ATACATGTTTACAGGATATTTGATTTCTGTTGCTGATATCTGTTTTCGACGAGTGCC 1487
QY 1141 GAGGCTACGTGGTCTACATTTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
DB 1488 GAGGCTACGTGGTCTACATTTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1547
QY 1201 GTTGTGGTGGAAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
DB 1548 GTTGTGGTGGAAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1607
QY 1261 GGAGTGTAGGAGAGGGCTGGTTTATGTTATGGGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1608 GGAGTGTAGGAGAGGGCTGGTTTATGTTATGGGGAGGAGTAGTTTACATAGGGGTC 1667
QY 1321 ATAGTGTAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC 1380
DB 1668 ATAGTGTAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAGATAACAGCACTGGAGCC 1727
QY 1381 CACTCCCTGTCACTGGGTGATCGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTGTCACTGGGTGATCGGGAGCAGGGCCAG 1767
RESULT 10
AA35379
ID AA35379 standard; DNA; 1767 BP.
XX
XX AAX35379;
XX
XX 07-JUL-1999 (first entry)
XX
XX Nucleotide sequence of PCV isolate Impl011-48285.
XX
XX PCV isolate; type II porcine circovirus; PCV; PMWS;
XX porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX
XX Porcine circovirus.
XX
XX WO918214-A1.
XX
XX 15-APR-1999.
XX
XX 01-OCT-1998; 98WO-FR002107.
PF

XX 03-OCT-1997; 97FR-00012382.
 PR 22-JAN-1998; 98FR-00000873.
 PR 20-MAR-1998; 98FR-00003707.
 XX (MERI-) MERIAL.
 PA (UYBE-) UNIV QUEBENS BELFAST.
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX Allan G, Meehan B, Clark E, Ellis J, Haines D, Haseard L;
 PI Harding J, Charreyre CE, Chappuis GE;
 XX WPI; 1999-264024/22.
 DR New type II porcine circovirus.
 XX Claim 11; Fig 2; 56pp; French.
 PS
 CC The present sequence represents the nucleotide sequence of PCV isolate
 CC Impl011-48285. The specification describes a preparation of type II
 CC porcine circovirus (PCV), which is particularly isolated from a lesion,
 CC from a pig with symptoms of PMWS (porcine multisystemic wasting
 CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,
 CC and vectors that express these polypeptides are all useful in vaccines,
 CC suitable for administration to adult or young pigs, or to pregnant sows
 CC (for passive immunization of their offspring). DNA isolated from PCV is
 CC used for in vivo or in vitro expression of viral polypeptides, also as
 CC probes or primers for diagnosis in usual hybridization or amplification
 CC assays. These polypeptides may also be used diagnostically to detect PCV-
 CC specific antibodies, while antibodies raised against the polypeptides can
 CC be used to detect antigens, in any usual immunoassay format
 CC
 XX Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;
 SQ
 Query Match 79.8%; Score 1410.4; DB 2; Length 1767;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ACCAGGCACTTCGGGAGGGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 60
 DB 348 ACCAGGCACTTCGGGAGGGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 407
 QY 61 AGAAGATGGAAGAGCGGAGCCCAACCCCAATAGGAGTGGGTCTCACTCTGTAATATC 120
 DB 408 AGAAGATGGAAGAGCGGAGCCCAACCCCAATAGGAGTGGGTCTCACTCTGTAATATC 467
 QY 121 CTTCCGAAGACGAGCGCAAGAAATAACGGATCTTCCCAATATCCCTATTTGATATTTTA 180
 DB 468 CTTCCGAAGACGAGCGCAAGAAATAACGGATCTTCCCAATATCCCTATTTGATATTTTA 527
 QY 181 TTGTTGGCGAGGAGGTATGAGGAGGAGCAGCAGCCTCAGGAGTGGGTCTCACTCTGTAAT 240
 DB 528 TTGTTGGCGAGGAGGTATGAGGAGGAGCAGCAGCCTCAGGAGTGGGTCTCACTCTGTAAT 587
 QY 241 TTGTTGAAGAGCAGACTTTTAAAGTGAAGTGGGTATTTGGGTGCGGCTGCCACATCG 300
 DB 588 TTGTTGAAGAGCAGACTTTTAAAGTGAAGTGGGTATTTGGGTGCGGCTGCCACATCG 647
 QY 301 AGAAGCGAAGAAAGACAGATCAGCAGAAATAAGATACTGCGAGTAAAGAGGCAACTTAC 360
 DB 648 AGAAGCGAAGAAAGACAGATCAGCAGAAATAAGATACTGCGAGTAAAGAGGCAACTTAC 707
 QY 361 TGAATGAGTGTGGAGCTCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGTGTGA 420
 DB 708 TGAATGAGTGTGGAGCTCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGTGTGA 767
 QY 421 GTACCTTGTGTGAGAGCGGAGTCTGTGTGACCCGTTCGAGAGCAGCAGCCTGTAAAGTTG 480
 DB 768 GTACCTTGTGTGAGAGCGGAGTCTGTGTGACCCGTTCGAGAGCAGCAGCCTGTAAAGTTG 827
 QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCGAGAGCGTG 540
 DB 828 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCGAGAGCGTG 887

QY 541 ATTGGAAGACTAATGTACACGTCAATTGTGGGGCCACCTGGGTGTGTGTAACCAATGGG 600
 DB 888 ATTGGAAGACTAATGTACACGTCAATTGTGGGGCCACCTGGGTGTGTGTAACCAATGGG 947
 QY 601 CTGCTAAATTTTCAGACCCCGGAAACACATACCTGGAACACCACTAGAAACAAGTGGTGG 660
 DB 948 CTGCTAAATTTTCAGACCCCGGAAACACATACCTGGAACACCACTAGAAACAAGTGGTGG 1007
 QY 661 ATGGTTACCATGGTGAAGAGTGGTGTATTTATGATGACCTTTATGGCTGGCTGGCTGGG 720
 DB 1008 ATGGTTACCATGGTGAAGAGTGGTGTATTTATGATGACCTTTATGGCTGGCTGGCTGGG 1067
 QY 721 ATGATCTACTGAGACTGTGTGATCCGATATCCATTTGATCTGAGAGACTAAAGGTGGAACTG 780
 DB 1068 ATGATCTACTGAGACTGTGTGATCCGATATCCATTTGATCTGAGAGACTAAAGGTGGAACTG 1127
 QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTGGAAATGTACT 840
 DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTGGAAATGTACT 1187
 QY 841 CCTCAACTGTGTCAGAGCTGTAGAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 900
 DB 1188 CCTCAACTGTGTCAGAGCTGTAGAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 1247
 QY 901 GGAAGATGCTACAGAAACAATCCAGGAGGAGGGGCCAGTTCTGTCACCCCTTTCCCGCC 960
 DB 1248 GGAAGATGCTACAGAAACAATCCAGGAGGAGGGGCCAGTTCTGTCACCCCTTTCCCGCC 1307
 QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTCTTTTATCACTTCTGTAATGGT 1020
 DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTCTTTTATCACTTCTGTAATGGT 1367
 QY 1021 TTTTATTTATTTAAGGGTTAAGTGGGGGTCTTTAAATTAATAATCTCTGAATGTAC 1080
 DB 1368 TTTTATTTATTTAAGGGTTAAGTGGGGGTCTTTAAGATTAATAATCTCTGAATGTAC 1427
 QY 1081 ATACATGGTTTACCGGATATTTATTTCTGCTGCTATATCTGTTTTCGAACCGAGTGGC 1140
 DB 1428 ATACATGGTTTACCGGATATTTATTTCTGCTGCTATATCTGTTTTCGAACCGAGTGGC 1487
 QY 1141 GAGGCTTACGTGCTATATTTCCAGCAGTTTCTAGTCTCAGCCACAGCTGGTTCCTTTT 1200
 DB 1488 GAGGCTTACGTGCTATATTTCCAGCAGTTTCTAGTCTCAGCCACAGCTGATTTCTTTT 1547
 QY 1201 GTTCTTTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260
 DB 1548 GTTCTTTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607
 QY 1261 GGAGTGTAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTAGTATTAATAGGGGTC 1320
 DB 1608 GGAGTGTAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTAGTATTAATAGGGGTC 1667
 QY 1321 ATAGGTAGGGCTGTGGCTTGTACAAAGTATATCATCTAAATAAATACAGCAGCTGGAGCC 1380
 DB 1668 ATAGGTAGGGCTGTGGCTTGTACAAAGTATATCATCTAGATAATAACAGCAGCTGGAGCC 1727
 QY 1381 CACTCCCCCTGTCAACCTGGGTGATCGGGGAGGAGGCGCAG 1420
 DB 1728 CACTCCCCCTGTCAACCTGGGTGATCGGGGAGGAGGCGCAG 1767

RESULT 11

AA35211
 ID AA35211 standard; DNA; 1767 BP.

XX AC AA35211;

XX DT 01-JUL-1999 (first entry)

XX DE Nucleotide sequence of PCV isolate Imp1011-48285.

XX KW PCV isolate; type II porcine circovirus; PCV; PMWS;

porcine multisystemic wasting syndrome; pig; vaccine; ss.

KW porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX Porcine circovirus.
OS PR2769322-Al.
PN XX
PD 09-APR-1999.
XX 22-JAN-1998; 98PR-00000873.
XX 03-OCT-1997; 97PR-00012382.
PR (MERI-) MERIAL SAS.
XX Allan G, Meehan B, Clark E, Ellis J, Haines D, Hassard L;
PI Harding J, Charreyre CE, Chappuis GE;
XX WPI; 1999-246948/21.
XX New type II porcine circovirus, used for, e.g. passive immunization of
PT pregnant sows.
XX Claim 14; Fig 2; 48pp; French.
XX The present sequence represents the nucleotide sequence of PCV isolate
CC Imp1011-48285. The specification describes a preparation of type II
CC porcine circovirus (PCV), which is particularly isolated from a lesion,
CC from a pig with symptoms of PMS (porcine multisystemic wasting
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,
CC and vectors that express these polypeptides are all useful in vaccines,
CC (for passive immunization of adult or young pigs, or to pregnant sows
CC (for passive immunization of their offspring). DNA isolated from PCV is
CC used for in vivo or in vitro expression of viral polypeptides, also as
CC probes or primers for diagnosis in usual hybridization or amplification
CC assays. These polypeptides may also be used diagnostically to detect PCV-
CC specific antibodies, while antibodies raised against the polypeptides can
CC be used to detect antigens, in any usual immunoassay format
XX
SQ Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;

Query Match 79.8%; Score 1410.4; DB 2; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGGCAGCGGAGCAGCACCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGGCAGCGGAGCAGCACCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 407

QY 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 120
DB 408 AGAAGAAATGGAAGAGCGGAGCAGCACCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 467

QY 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGTAATTTTA 180
DB 468 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGTAATTTTA 527

QY 181 TTGTTGGCAGGAGGGTAATGAGAGGAGGAGCAGCACCCTCAGCAGGGGTTCGCTAAAT 240
DB 528 TTGTTGGCAGGAGGGTAATGAGAGGAGGAGCAGCACCCTCAGCAGGGGTTCGCTAAAT 587

QY 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGGTGCCCGTCGCACATCG 300
DB 588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGGTGCCCGTCGCACATCG 647

QY 301 AGAAGCGAAGGAAACAGATCAGCAGAAATAAGAAATACCTGACGTAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGGAAACAGATCAGCAGAAATAAGAAATACCTGACGTAAGAGGCAACTTAC 707

QY 361 TGATGGAGTGGAGCTCCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGCTGTGA 420
DB 708 TGATGGAGTGGAGCTCCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGCTGTGA 767

QY 421 GTACCTTGTGGAGAGCGGGAGTCTGTTGACCGTTGTCAGAGCAGCACCCTGTAAACGTTTG 480

RESULT 12
AAZ56870
ID AAZ56870 standard; DNA; 1767 BP.
XX
AC AAZ56870;

DB 768 GTACCTTGTGGAGAGCGGAGTCTGGTGACCGTTGCAGACAGCACCCTGTAAACGTTTG 827
QY 481 TCAGAAATTTCCCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATTCAGAGACGCTG 540
DB 828 TCAGAAATTTCCCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATTCAGAGACGCTG 887
QY 541 ATTGGAAGACTAATGTACACCTCACTGTGGGGCCACCTGGGTGTGGTAAAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACACCTCACTGTGGGGCCACCTGGGTGTGGTAAAAAGCAATGGG 947
QY 601 CTGCTAATTTTGCAGACCCGGAACCATACATCTGAAACCCACCTAGAAACCAAGTGGTGG 660
DB 948 CTGCTAATTTTGCAGACCCGGAACCATACATCTGAAACCCACCTAGAAACCAAGTGGTGG 1007
QY 661 ATGGTTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 1008 ATGGTTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067
QY 721 ATGATCTACTCAGACTGTGTGATCGATATCGATATCGATATCGATATCGATATCGATATCG 780
DB 1068 ATGATCTACTCAGACTGTGTGATCGATATCGATATCGATATCGATATCGATATCGATATCG 1127
QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTACGCAATCAGACCCCGTTGGAATGCTACT 840
DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTACGCAATCAGACCCCGTTGGAATGCTACT 1187
QY 841 CCTCAACTGCTGTCACGCTGTAGAAAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 1188 CCTCAACTGCTGTCACGCTGTAGAAAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 1247
QY 901 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGGCAGTTCACCTTTCCCTCC 960
DB 1248 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGGCAGTTCACCTTTCCCTCC 1307
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1367
QY 1021 TTTTATTTTCAATTAAGGTTAAAGTGGGGGTCTTTAAAAATTAATTAATTAATTAATTAAT 1080
DB 1368 TTTTATTTTCAATTAAGGTTAAAGTGGGGGTCTTTAAAAATTAATTAATTAATTAATTAAT 1427
QY 1081 ATACATGGTTTACACGGATATTTGATTTCTCTGGTGTATATATCTGTTTTCGAAACGCTG 1140
DB 1428 ATACATGGTTTACACGGATATTTGATTTCTCTGGTGTATATATCTGTTTTCGAAACGCTG 1487
QY 1141 GAGGCTTACGCTGTCTACATTTCCAGCAGTGTGTTAGTCTCAGCCACAGCTGGTTCCTTTT 1200
DB 1488 GAGGCTTACGCTGTCTACATTTCCAGTGTGTTAGTCTCAGCCACAGCTGGTTCCTTTT 1547
QY 1201 GTTGTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260
DB 1548 GTTGTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607
QY 1261 GGAGTGGTAGGAGAGGGCTGGGTATTTGATGGGGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1608 GGAGTGGTAGGAGAGGGCTGGGTATTTGATGGGGGAGGAGTAGTTTACATAGGGGTC 1667
QY 1321 ATAGTGGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCAGCTGGAGCC 1380
DB 1668 ATAGTGGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAGAAATTAACAGCAGCTGGAGCC 1727
QY 1381 CACTCCCTGTCCCTGGTGTATCGGGGAGCAGGSCCAG 1420
DB 1728 CACTCCCTGTCCCTGGTGTATCGGGGAGCAGGSCCAG 1767

XX 06-AUG-2003 (revised)
DT 18-MAY-2001 (first entry)
XX PCV DNA fragment of Imp 1011-48285 strain.
XX Vaccine; pig; myocarditis; abortion; intrauterine infection;
KW multisystemic wasting syndrome; ds.
XX Porcine circovirus type 2.
XX WO200116330-A2.
XX 08-MAR-2001.
XX 28-AUG-2000; 2000WO-EP008781.
XX 31-AUG-1999; 99US-0151564P.
XX 31-MAY-2000; 2000US-00583350.
XX (MERI-) MERIAL.
XX (UYSA-) UNIV SASKATCHEWAN.
XX (UYBE-) UNIV QUEENS BELFAST.
XX Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;
XX McNeill F;
XX WPI; 2001-244408/25.
XX Use of porcine circovirus-2 immunogen to formulate a vaccine composition
PT to treat pigs against myocarditis, abortion, intrauterine infection
PT and/or post-weaning, multisystemic wasting syndrome associated with PCV-
XX 2.
XX Disclosure; Fig 2 #2; 134pp; English.
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)
CC immunogen to formulate a vaccine composition to prevent or treat pigs
CC against myocarditis and/or abortion and/or intrauterine infection and/or
CC post-weaning, multisystemic wasting syndrome and other pathological
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of
CC a strain of PCV, which was used in the present invention. (Updated on 06-
XX AUG-2003 to correct OS field.)
XX Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;
Query Match 79.8%; Score 1410.4; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACCAGGCGACTTCGGGAGCGGAGACCTCGGAGGACCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGGCGACTTCGGGAGCGGAGACCTCGGAGGACCTCAGCAGCAACATGCCAGCA 407
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCATAAAGGTGGGTTCCTCTGAAATATC 120
DB 408 AGAAGATGGAAGAGCGGACCCCAACCCATAAAGGTGGGTTCCTCTGAAATATC 467
QY 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTTATTTA 180
DB 468 CTTCCGAGACGAGCGCAGAAATACGGGATCTTCCAATATCCCTATTGATTTATTTA 527
QY 181 TTGTTGCGAGGAGGTATAGGAAGGAGCAACCTCACCCTCGAGGGTTCGCTAAAT 240
DB 528 TTGTTGCGAGGAGGTATAGGAAGGAGCAACCTCACCCTCGAGGGTTCGCTAAAT 587
QY 241 TTGTTGAGAGCAGACTTTTAAATAGTGAAGTGGTATTGTTGGTCCCGCTGCCATCG 300
DB 588 TTGTTGAGAGCAGACTTTTAAATAGTGAAGTGGTATTGTTGGTCCCGCTGCCATCG 647
QY 301 AGAAGCGAAGGAAACAGATCAGCAATAAAGATCTCAGTAAAGAGGCAACTTAC 360

DB 648 AGAAGCGAAGGAAACAGATCAGCAATAAAGATCTCAGTAAAGAGGCAACTTAC 707
QY 361 TGATGGAGTGTGGAGCTCTAGATCTCAGGACAAACGAGTGAACCTGTCTACTGTGTA 420
DB 708 TGATGGAGTGTGGAGCTCTAGATCTCAGGACAAACGAGTGAACCTGTCTACTGTGTA 767
QY 421 GTACCTTGTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCCTGTAGCTTTG 480
DB 768 GTACCTTGTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCCTGTAGCTTTG 827
QY 481 TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGAGCGGGAATAATCAGAAAGCGTG 540
DB 828 TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGAGCGGGAATAATCAGAAAGCGTG 887
QY 541 ATTGGAAGACTAATGTACACGTCATTTGCGGCGCACCTGTGGTGTGTTAAAGCAAAATGG 600
DB 888 ATTGGAAGACTAATGTACACGTCATTTGCGGCGCACCTGTGGTGTGTTAAAGCAAAATGG 947
QY 601 CTGCTAATTTTGCAGACCCGGAACCATACTTGGAAACCACTTGAACCAAGTGGTGG 660
DB 948 CTGCTAATTTTGCAGACCCGGAACCATACTTGGAAACCACTTGAACCAAGTGGTGG 1007
QY 661 ATGTTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGG 720
DB 1008 ATGTTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAAC 780
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAAC 1127
QY 781 TACCTTTTGGCGCGAGTATCTGATACAGCAATCAGACCCGCTTGGATGGTACT 840
DB 1128 TACCTTTTGGCGCGAGTATCTGATACAGCAATCAGACCCGCTTGGATGGTACT 1187
QY 841 CCTCAACTGCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 1188 CCTCAACTGCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 1247
QY 901 GGAAGATGCTACAGAACAAATCCAGGAGGAGGGGCGCAGTTCGTACCCCTTTCCCCC 960
DB 1248 GGAAGATGCTACAGAACAAATCCAGGAGGAGGGGCGCAGTTCGTACCCCTTTCCCCC 1307
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTA 1020
DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAAT 1367
QY 1021 TTTTATTTATTAAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAAT 1080
DB 1368 TTTTATTTATTAAGGTTAAGTGGGGGCTTTTAAAGTAAATTAATTAATTAATTAATTA 1427
QY 1081 ATACATGTTTACACGATATTTATTTCTGTTGCTGATATATCTGTTTTCGAAGCGAGTGC 1140
DB 1428 ATACATGTTTACACGATATTTATTTCTGTTGCTGATATATCTGTTTTCGAAGCGAGTGC 1487
QY 1141 GAGGCTACGTTCTACATTTCCAGCACTTTGATGTTCTCAGCAGCAGCTGTTTCTTTT 1200
DB 1488 GAGGCTACGTTCTACATTTCCAGCACTTTGATGTTCTCAGCAGCAGCTGTTTCTTTT 1547
QY 1201 GTTGTGTTGTTGGAAGTAACTAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260
DB 1548 GTTGTGTTGTTGGAAGTAACTAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607
QY 1261 GGAGTGTAGGAGAGGGGCTGGTGTATGTTATGGTGGGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1608 GGAGTGTAGGAGAGGGGCTGGTGTATGTTATGGCGGAGGAGTAGTTTACATAGGGGTC 1667
QY 1321 ATAGGTGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATTAACAGCACTGAGCC 1380
DB 1668 ATAGGTGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAGAAATAACAGCACTGAGCC 1727
QY 1381 CACTCCCTGTCAACCTCGGTTGATCGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTGTCAACCTCGGTTGATCGGGAGCAGGGCCAG 1767

RESULT 14
ID AAX35381
XX AAX35381 standard; DNA; 1768 BP.
XX
XX
XX AAX35381;
XX
XX 07-JUL-1999 (first entry)
XX
XX Nucleotide sequence of PCV isolate Imp1010.
XX
XX PCV isolate; type II porcine circovirus; PCV; PMWS;
XX porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX
XX Porcine circovirus.
XX
XX OS
XX PN W09918214-A1.
XX
XX PD 15-APR-1999.
XX
XX PF 01-OCT-1998; 98WO-FR002107.
XX
XX PR 03-OCT-1997; 97ER-00012382.
XX
XX PR 22-JAN-1998; 98FR-00000873.
XX
XX PR 20-MAR-1998; 98FR-00003707.
XX
XX (MERI-) MERIAL.
XX PA (UYBE-) UNIV QUEENS BELFAST.
XX PA (UYSA-) UNIV SASKATCHEWAN.
XX
XX PI Allan G, Meehan B, Clark E, Ellis J, Haines D, Hassard L;
XX PI Harding J, Charreyre CE, Chappuis GE;
XX
XX DR WPI; 1999-264024/22.
XX
XX PT New type II porcine circovirus.
XX
XX PS Claim 11; Fig 4; 56pp; French.
XX
XX The present sequence represents the nucleotide sequence of PCV isolate
CC Imp1010. The specification describes a preparation of type II porcine
CC circovirus (PCV), which is particularly isolated from a lesion, from a
CC pig with symptoms of PMWS (porcine multisystemic wasting syndrome). PCV
CC (attenuated or inactivated); polypeptides derived from it, and vectors
CC that express these polypeptides are all useful in vaccines, suitable for
CC administration to adult or young pigs, or to pregnant sows (for passive
CC immunization of their offspring). DNA isolated from PCV is used for in
CC vivo or in vitro expression of viral polypeptides, also as probes or
CC primers for diagnosis in usual hybridization or amplification assays.
CC These polypeptides may also be used diagnostically to detect PCV-specific
CC antibodies, while antibodies raised against the polypeptides can be used
CC to detect antigens, in any usual immunoassay format
XX
XX SQ Sequence 1768 BP; 451 A; 361 C; 495 G; 461 T; 0 U; 0 Other;

Query Match 75.6%; Score 1335.4; DB 2; Length 1768;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 1 ACCAGGCGCACTTCGGCAGCGGCGAGCACCTCGGCGAGCACCTCAGCAGCAACATGCCGAGCA 60
DB 348 ACCAGGCGCACTTCGGCAGCGGCGAGCACCTCGGCGAGCACCTCAGCAGCAACATGCCGAGCA 407
QY 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAGGTGGGTTCACCTCTGAATAATC 120
DB 408 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAGGTGGGTTCACCTCTGAATAATC 467
QY 121 CTTCCGAGACGAGCCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA 180
DB 468 CTTCCGAGACGAGCCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA 527
QY 181 TTGTTGGCAGGAGGGTAAATGAGGAAGGACCAACCTCACCTCCAGGGGTTCGCTAAATT 240

DB 528 TTGTTGGCAGGAGGGTAAATGAGGAAGGACCAACCTCACCTCCAGGGGTTCGCTAAATT 587
QY 241 TTGTTGAGGAGCAGACTTTTAAATAAGTGAAGTGTATTGGGTGCTCCGCTCCACATCG 300
DB 588 TTGTTGAGGAGGCAAACTTTTAAATAAGTGAAGTGTATTGGGTGCTCCGCTCCACATCG 647
QY 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATCTGCACTAAAGAGCAACTTAC 360
DB 648 AGAAGCGAAAGGAACTGATCAGCAGAAATAAAGAAATATTGCACTAAAGAGCAACTTAC 707
QY 361 TGATGAGTGTGAGCTCTAGATCTCAGGAGCAACGAGTGCACCTGTCTACTGTGCTGA 420
DB 708 TTATTGAATGTGAGCTCTCGATCTCAAGGAAACGAGTGCACCTGTCTACTGTGCTGA 767
QY 421 GTACCTTGTGAGAGCGGAGTCTGGTGCACCGTTGCAGAGCAGCACCCTGTAAACGTTTG 480
DB 768 GTACCTTGTGAGAGCGGAGTCTGGTGCACCGTTGCAGAGCAGCACCCTGTAAACGTTTG 827
QY 481 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATAATGCAGAGCGTG 540
DB 828 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATAATGCAGAGCGTG 887
QY 541 ATTGGAAGACTAATGTACAGTCACTTGTGGGCGCACCTGGGTGTGTTAAAGCAATGCG 600
DB 888 ATTGGAAGACCAATGTATACAGCTCATTTGTGGGCGCACCTGGGTGTGTTAAAGCAATGCG 947
QY 601 CTGCTAATTTTGCAGACCCCGGAAACACATATCTGGAACACCTAGAAACAAAGTGTGGG 660
DB 948 CTGCTAATTTTGCAGACCCCGGAAACACATATCTGGAACCACTAGAAACAAAGTGTGGG 1007
QY 661 ATGTTTACCATGTGGAAGTGGTTGTTATTGATGACTTTTATGCTGGCTGGCTCCCTGGG 720
DB 1008 ATGTTTACCATGTGGAAGTGGTTGTTATTGATGACTTTTATGCTGGCTGGCTCCCTGGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAAC 780
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAAC 1127
QY 781 TACCTTTTGGCGCGCAGTATTCTGATTACCAACAATCAGACCCCGTTGGAAATGTTACT 840
DB 1128 TACCTTTTGGCGCGCAGTATTCTGATTACCAACAATCAGACCCCGTTGGAAATGTTACT 1187
QY 841 CCTCAACTGTGTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 1188 CCTCAACTGTGTCCAGCTGTAGAGCTCTCTATCGGAGGATTAATCTCTTGGTATTTT 1247
QY 901 GGAAGATGTCTACAGAACAAATCCAGGAGGAGGGGCGCAGTTTCGTCAACCTTTTCCCGCC 960
DB 1248 GGAAGATGTCTACAGAACAAATCCAGGAGGAGGGGCGCAGTTTCGTCAACCTTTTCCCGCC 1307
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1367
QY 1021 TTTTATTATTATTAAGG--TTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTA 1079
DB 1368 TTTTATTATTATTAAGGTTTAAAGTGGGGGCTTTTAAAGTAAATTAATTAATTAATTAATTA 1427
QY 1080 CATACATGTTTACACGAGATTTGTTATTCCTGCTGATATATCTGTTTTCGAACGAGTGC 1139
DB 1428 CATACATGTTTACACGAGATTTGTTATTCCTGCTGATATATCTGTTTTCGAACGAGTGC 1487
QY 1140 CGAGGCTTACGTGTCTACATTTCCAGAGTGTGTAGTCTCAGCAACAGTGTGTTCTTT 1199
DB 1488 CGAGGCTTACGTGTCTACATTTCCAGAGTGTGTAGTCTCAGCAACAGTGTGTTCTTT 1547
QY 1200 TGTGTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTCGGGTTAAAGTACC 1259
DB 1548 TGTGTTGTTGGAAGTAAATCAATAGTGAAGTCAAGAACAGGTTTCGGGTTGAGTAAAC 1607
QY 1260 GGGAGTGTAGGAGAGGGCTGTTATGTTATGGCGGGAGGAGTAGTTTACATAGGGGT 1319

Db 1608 GGGAGTGGTAGGAGAGGGTTGGGGATTGTATGCGGGAGAGTAGTTTACATATGGGT 1667
QY 1320 CATAGTGTAGGGCTGTGGCTTTGTTCAAAAGTTATCATCTAAAATAACAGCACTGGAGC 1379
Db 1668 CATAGTGTAGGGCTGTGGCTTTGTTCAAAAGTTATCATCTAGATATACAGCAGTGGAGC 1727
QY 1380 CCATCTCCCTGTACCCCTGGGTGATCGGGGAGCAGGGCCAG 1420
Db 1728 CCATCTCCCTATCACCTGGGTGATGGGGAGCAGGGCCAG 1768

RESULT 15

AA35380
ID AAX35380 standard; DNA; 1768 BP.
XX
AC AAX35380;
XX
XX
DT 07-JUL-1999 (first entry)
XX
DE Nucleotide sequence of PCV isolate Imp999 (corrected version).
XX
XX PCV isolate; type II porcine circovirus; PCV; PMWS;
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.
XX
XX Porcine circovirus.
OS
PN WO9118214-A1.
XX
XX
PD 15-APR-1999.
XX
XX 01-OCT-1998; 98WO-FR002107.
XX
XX
PR 03-OCT-1997; 97PR-00012382.
PR 22-JAN-1998; 98PR-00000873.
PR 20-MAR-1998; 98PR-00003707.
XX
XX (MERI-) MERIAL.
PA (UYBE-) UNIV QUEENS BELFAST.
PA (UYSA-) UNIV SASKATCHEWAN.

XX
PI Allan G, Meehan B, Clark E, Ellis J, Haines D, Haesard L;
PI Harding J, Charreyre CE, Chappuis GE;
XX WPI; 1999-264024/22.
XX
XX New type II porcine circovirus.
XX
XX Claim 11; Fig 3; 56pp; French.

CC The present sequence represents the nucleotide sequence of PCV isolate
CC Imp999. The specification describes a preparation of type II porcine
CC circovirus (PCV), which is particularly isolated from a lesion, from a
CC pig with symptoms of PMWS (porcine multisystemic wasting syndrome). PCV
CC (attenuated or inactivated), polypeptides derived from it, and vectors
CC that express these polypeptides are all useful in vaccines, suitable for
CC administration to adult or young pigs, or to pregnant sows (for passive
CC immunization of their offspring). DNA isolated from PCV is used for in
CC vivo or in vitro expression of viral polypeptides, also as probes or
CC primers for diagnosis in usual hybridization or amplification assays.
CC These polypeptides may also be used diagnostically to detect PCV-specific
CC antibodies, while antibodies raised against the polypeptides can be used
CC to detect antigens, in any usual immunoassay format

XX SQ Sequence 1768 BP; 453 A; 360 C; 494 G; 461 T; 0 U; 0 Other;

Query Match 75.6%; Score 1335.4; DB 2; Length 1768;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 1 ACCAGCGCACTTCGGCAGCGGAGCACCCTCGGAGCAGCACTTCAGCAGCAATGCCAGCA 60
Db 348 ACCAGCGCACTTCGGCAGCGGAGCACCCTCGGAGCAGCACTTCAGCAGCAATGCCAGCA 407

QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGATATATC 120
Db 408 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGATATATC 467
QY 121 CTTCCGAAGACGACGCGAAGAAATACGGGATCTTCAATATCCCTATTTGATATATTTTA 180
Db 468 CTTCCGAAGACGACGCGAAGAAATACGGGAGCTCCCAATCTCCCTATTTGATATATTTTA 527
QY 181 TTGTTGGCGAGGAGGTAAATGAGGAAGGACGAAACACCTCACCTCAGGGGTTCGTAATTT 240
Db 528 TTGTTGGCGAGGAGGTAAATGAGGAAGGACGAAACACCTCACCTCAGGGGTTCGTAATTT 587
QY 241 TTGTAAGAAGCAGACTTTTAAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Db 588 TTGTAAGAAGCAGACTTTTAAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 647
QY 301 AGAAAGCGAAAGGAAACAGATCAGCAGATAAAGAAATACTGCAGTAAAGAGCAACTTAC 360
Db 648 AGAAAGCGAAAGGAACTGATCAGCAGATAAAGAAATATTTGCAGTAAAGAGCAACTTAC 707
QY 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGACCAACGAGTGACCTGTCTACTGTGTGA 420
Db 708 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACCAACGGAGTGACCTGTCTACTGTGTGA 767
QY 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCTGTAAAGTTTG 480
Db 768 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCTGTAAAGTTTG 827
QY 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGCAGCGGAAATATGCAAGACGCTG 540
Db 828 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGCAGCGGAAATATGCAAGACGCTG 887
QY 541 ATTGGAAGACTAAATGTACACGTCATTGTGGGGCCACCTGGGTGTGTTAAAAGCAAAATGGG 600
Db 888 ATTGGAAGACCAATGTACACGTCATTGTGGGGCCACCTGGGTGTGTTAAAAGCAAAATGGG 947
QY 601 CTGCTAAATTTTCAGACCCCGGAAACCATACTTGAAGAACCCCTAGAAACCAAGTGGTGGG 660
Db 948 CTGCTAAATTTTCAGACCCCGGAAACCATACTTGAAGAACCCCTAGAAACCAAGTGGTGGG 1007
QY 661 ATGGTTACCATGTCGAAGAGTGGTGTATTGATGACTTTTTATGGCTGGCTGCCCTGGG 720
Db 1008 ATGGTTACCATGTCGAAGAGTGGTGTATTGATGACTTTTTATGGCTGGCTGCCCTGGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACTG 780
Db 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACTG 1127
QY 781 TACCTTTTTTGGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTGGGAATGCTACT 840
Db 1128 TACCTTTTTTGGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTGGGAATGCTACT 1187
QY 841 CCTCAACTGCTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
Db 1188 CCTCAACTGCTCTCCAGCTGTAGAGCTCTCTATCGGAGGATTAATCTCTTGGTATTTT 1247
QY 901 GGAAGAAATCTCAGAAACAATCCAGGAGAAAGGGGGCCAGTTCCGTCAACCTTTCCCCC 960
Db 1248 GGAAGAAATCTCAGAAACAATCCAGGAGAAAGGGGGCCAGTTCCGTCAACCTTTCCCCC 1307
QY 961 CATGCCCTGAATTTCCATATGAAATAAATACCTAGTCTTTTTTATCACTGCTGTAATGTT 1020
Db 1308 CATGCCCTGAATTTCCATATGAAATAAATACCTAGTCTTTTTTATCACTGCTGTAATGTT 1367
QY 1021 TTTTATTTTCAATTAAGGG-TTAAGTGGGGGCTCTTTAAATAAATTAATCTCTGAAATGTA 1079
Db 1368 TTTTATTTTCAATTAAGGGTTAAGTGGGGGCTCTTTAAGATTAATAATCTCTGAAATGTA 1427
QY 1080 CATACATGTTTACACGGATATTGTATTCTCTGGTCGTATATCTGTTTTTTCGAAACGAGTGC 1139
Db 1428 CATACATGTTTACACGGATATTGTACTCTCTGGTCGTATATCTGTTTTTTCGAAACGAGTGC 1487
QY 1140 CGAGGCTACGTGGTCTACATTTTCCAGAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1199

Db 1488 CGAGCCCTACGTGTCACATTTCTAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCTTT 1547
Qy 1200 TGTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC 1259
Db 1548 TGTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGGAAGTAAC 1607
Qy 1260 GGGAGTGTAGGAGAGGGCTGGGTTATGGTATGCGCGGAGGAGTACTTTACATAGGGGT 1319
Db 1608 GGGAGTGTAGGAGAGGGTTGGGGGATTGTATGCGCGGAGGAGTACTTTACATAGGGGT 1667
Qy 1320 CATAGGTCAGGGCTGTGGCCCTTGTACAAAGTTTATCATCTAAATTAACAGCACTGGAGC 1379
Db 1668 CATAGGTTAGGGCTGTGGCCCTTGTACAAAGTTTATCATCTAGATTAACAGCACTGGAGC 1727
Qy 1380 CCACTCCCTCTCACCCCTGGGTGATCGGGGAGCAGGGCCAG 1420
Db 1728 CCACTCCCTATCACCCCTGGGTGATGGGGGAGCAGGGCCAG 1768

Search completed: December 7, 2004, 17:57:13
Job time : 880 secs